

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Scott, Matthew P.
Goodrich, Lisa V.
Johnson, Ronald L.
- (ii) TITLE OF INVENTION: Mammalian Patched Gene and Its Use
- (iii) NUMBER OF SEQUENCES: 20
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 - (B) STREET: 4 Embarcadero Center, Suite 3400
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94111-4187
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Rowland, Bertram I
 - (B) REGISTRATION NUMBER: 20,015
 - (C) REFERENCE/DOCKET NUMBER: A60190/BIR STAN171
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 781-1989
 - (B) TELEFAX: (415) 398-3249
 - (C) TELEX: 910277299

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 680 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AACCTATGGC ACCCCCCCCA ACCTTTCCTA ACAAACCC	TTTATACCCC CTAAATTTT	60
CCACCCAAAC CCTGAACAGA AACCTTTT	TAAACCCCA CCCGGAATTC CATCCCCC	120

AAATTACAAC TCCAGCCAAA ATTAAAATTG GTCCTAACCT AACCATGTTG TTACGGTTTC	180
CCCCCCCCAAA TACATGCACT GGCCCGAACA CTTGATCGTT GCCGTTCCAA TAAGAATAAA	240
TCTGGTCATA TTAAACAAGC CAAAGCTTTA CAAACTGTTG TACAATTAAT GGGCGAACAC	300
GAACTGTTCG AATTCTGGTC TGGACATTAC AAAGTGCACC ACATCGGATG GAACCAGGAG	360
AAGGCCACAA CCGTACTGAA CGCCTGGCAG AAGAAGTTCG CACAGGTTGG TGGTTGGCGC	420
AAGGAGTAGA GTGAATGGTG GTAATTTTGT GTTGTTCCAG GAGGTGGATC GTCTGACGAA	480
GAGCAAGAAG TCGTCGAATT ACATCTTCGT GACGTTCTCC ACCGCCAATT TGAACAAGAT	540
GTTGAAGGAG GCGTCGAAAC GGACGTGGTG AAGCTGGGGG TGGTGCTGGG GGTGGCGGCG	600
GTGTACGGGT GGGTGGCCCA GTCGGGGCTG GCTGCCTTGG GAGTGCTGGT CTTGCGGCTC	660
ATTCGCCCTA TAGTAGCGTA	680

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa	Pro	Pro	Pro	Asn	Tyr	Asn	Ser	Xaa	Pro	Lys	Xaa	Xaa	Xaa	Leu	Val	1	5	10	15
Leu	Thr	Pro	Xaa	Val	Val	Thr	Val	Ser	Pro	Pro	Lys	Tyr	Met	His	Trp	20	25	30	
Pro	Glu	His	Leu	Ile	Val	Ala	Val	Pro	Ile	Arg	Ile	Asn	Leu	Val	Ile	35	40	45	
Leu	Asn	Lys	Pro	Lys	Ala	Leu	Gln	Thr	Val	Val	Gln	Leu	Met	Gly	Glu	50	55	60	
His	Glu	Leu	Phe	Glu	Phe	Trp	Ser	Gly	His	Tyr	Lys	Val	His	His	Ile	65	70	75	80
Gly	Trp	Asn	Gln	Glu	Lys	Ala	Thr	Thr	Val	Leu	Asn	Ala	Trp	Gln	Lys	85	90	95	
Lys	Phe	Ala	Gln	Val	Gly	Gly	Trp	Arg	Lys	Glu						100	105		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4448 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCCAGTGTC GACACGCTGT TAAGGTGTTA CGAAACTATC GAAACTCTGT ACCGTTCCGT	60
GTTACATTCG GTCAGTGATA AACAGAAGTG AATAATTCGG GTGTACAAGT GTGTGGTTAT	120
GTGGCGGCGA GTGATATGAC AGCGTGCGCC GCCAGACGGA TTCCAGCCGT CTCATGAGG	180
ATATCGGTGA CAAGCCTGGC CCCGAGATCA TGGTGGCTCC CGATTCCGAG GCTCCTTCGA	240
ATCCTCGGAT AACGGCTGCA CACGAGAGCC CCTGCGCCAC CGAGGCGCGC CACAGTGCTG	300
ATCTTTACAT ACGTACCAGT TGGGTGGACG CCGCACTAGC TCTCTCTGAA CTCGAAAAGG	360
GTAACATCGA AGGAGGAAGA ACCTCTCTGT GGATACGAGC GTGGCTACAA GAACAGCTCT	420
TTATTTTGGG CTGCTTTCTT CAAGGCGACG CGGGGAAAGT CCTCTTCGTT GCCATCCTCG	480
TTCTGTGCGAC GTTCTGCGTC GGTCTCAAGT CAGCACAAAT ACATACAAGG GTCGACCAAC	540
TCTGGGTTCA AGAGGGTGGT AGATTAGAAG CCGAGTTGAA ATATACAGCG CAAGCTTTGG	600
GCGAGGCGGA CTCCTCGACG CACCAGCTTG TCATACAAAC TGCCAAAGAT CCAGACGTCT	660
CCCTGCTACA TCCAGGCGCG TTGCTTGAAC ACCTTAAGGT GGTGCACGCA GCGACTCGGG	720
TGACAGTTCA CATGTACGAC ATTGAGTGGC GCCTCAAAGA CCTGTGCTAC AGCCCCAGCA	780
TACCGGACTT CGAGGGTTAC CACCACATCG AGTCAATCAT AGACAACGTC ATCCCCTGCG	840
CTATTATCAC CCCCTTGAT TGCTTCTGGG AAGGCTCCAA GTTGCTTGGT CCCGATTATC	900
CTATATACGT ACCACATCTT AAACACAAAC TACAATGGAC ACATTTAAAT CCATTGGAAG	960
TTGTAGAAGA AGTGAAAAAA TTAAAGTTCC AATTTCTCTT GAGCACAATA GAGGCGTACA	1020
TGAAGAGAGC CGGCATCACT TCCGCCTACA TGAAAAAGCC GTGCTTAGAC CCCACCGACC	1080
CACATTGTCC AGCCACGGCT CCAAACAAAA AGTCTGGTCA TATTCCAGAT GTAGCGGCGG	1140
AGCTGTCGCA CGGATGTTAT GGTTTCGCGG CAGCTTACAT GCACTGGCCG GAACAGTTAA	1200
TTGTAGGGGG AGCTACAAGG AATTCGACAT CAGCTCTGAG AAAAGCACGC GTTTACAGAC	1260
TGTAGTACAG TTAATGGGCG AGAGAGAAAT GTACGAGTAC TGGGCCGATC ATTATAAAGT	1320
ACATCAAATT GGCTGGAATC AAGAGAAGGC AGCTGCTGTA CTGGATGCCT GGCAGAGAAA	1380
GTTTGCCGCT GAAGTCAGAA AAATTACTAC CTCAGGATCA GTATCATCGG CTTATAGTTT	1440

CTATCCGTTT	TCCACCTCGA	CACTTAATGA	CATACTCGGG	AAGTTCTCCG	AAGTGTCACT	1500
GAAGAACATT	ATATTAGGCT	ATATGTTTAT	GTTAATTTAT	GTTGCCGTTA	CTTTAATACA	1560
ATGGCGGGAT	CCGATTGCT	CGCAAGCGGG	TGTGGGTATC	GCCGGAGTTC	TACTACTATC	1620
AATCACTGTT	GCCGCTGGCT	TAGGATTTTG	TGCTTTATTA	GGCATAACAT	TCAACGCTTC	1680
AAGTACGCAA	ATAGTACCAT	TCCTAGCGCT	CGGGTTAGGA	GTTCAAGATA	TGTTTCTTCT	1740
CACTCACACG	TATGTGGAGC	AAGCGGGAGA	TGTGCCTAGA	GAAGAGAGGA	CTGGACTTGT	1800
ATTGAAAAAG	AGCGGTTTAA	GCGTACTTCT	GGCGTCTTTG	TGCAACGTGA	TGGCATTTTT	1860
GGCAGCAGCC	CTTCTACCTA	TTCCAGCTTT	CAGAGTATTT	TGCCTACAGG	CTGCCATACT	1920
TCTTCTGTTT	AACTTGGGGT	CAATATTACT	GGTTTTTCCT	GCTATGATCT	CGTTAGACCT	1980
GCGACGGAGG	TCAGCCGCGA	GGGCCGATCT	TTTATGCTGT	TTGATGCCTG	AGAGTCCATT	2040
ACCGAAGAAG	AAAATTCCGG	AAAGAGCAAA	AACTAGAAAA	AACGATAAGA	CTCATAGGAT	2100
AGACACCACG	AGACAACCTC	TAGACCCAGA	TGTGTCCGAG	AACGTGACCA	AAACTTGCTG	2160
CTTAAGCGTC	TCGCTCACCA	AGTGGGCCAA	GAACCAATAC	GCGCCGTTCA	TCATGCGCCC	2220
CGCTGTTAAG	GTTACATCCA	TGTTAGCGTT	GATTGCTGTT	ATTCTGACTA	GCGTTTGGGG	2280
AGCGACAAAA	GTAAAGGATG	GATTGGATTT	GACTGATATT	GTACCGGAGA	ATACAGACGA	2340
ACACGAATTT	TTATCTCGTC	AGGAAAAATA	CTTTGGCTTC	TATAATATGT	ACGCCGTGAC	2400
GCAAGGCAAC	TTTGAATATC	CCACCAATCA	GAAGTTATTA	TATGAGTATC	ACGATCAATT	2460
CGTCAGAATA	CCTAATATAA	TCAAGAATGA	TAACGGCGGT	CTCACGAAAT	TTTGGTTGAG	2520
TTTATTCCGC	GACTGGTTAT	TGGACTTGCA	AGTGGCTTTT	GATAAGGAGG	TTGCCAGCGG	2580
TTGTATAACA	CAAGAGTATT	GGTGCAAAAA	CGCGAGTGAC	GAAGGAATAT	TGGCCTATAA	2640
ACTTATGGTG	CAGACTGGCC	ATGTGGACAA	TCCAATCGAT	AAGTCTCTGA	TTACGGCAGG	2700
TCACAGACTA	GTTGACAAAG	ACGGTATTAT	AAATCCAAAG	GCATTTTATA	ATTACCTATC	2760
AGCTTGGGCT	ACTAACGACG	CGTTGGCATA	CGGAGCCTCA	CAAGGGAACT	TGAAACCTCA	2820
GCCCCAAAGA	TGGATCCATT	CTCCGGAGGA	TGTACATTTA	GAAATAAAGA	AATCGTCGCC	2880
ATTAATTTAC	ACACAGTTAC	CATTCTACCT	TTCCGGTCTC	AGCGACACTA	TAGCATCAAA	2940
ACGTTGATAA	GATCTGTGCG	AGATTTATGT	CTGAAGTACG	AGGCGAAAGG	TTTACCGAAC	3000
TTTCCATCGG	GTATACCATT	CCTTTTCTGG	GAACAGTATT	TGTATTTAAG	GACATCTTTA	3060
CTACTGGCTT	TGGCGTGTGC	TTTGGCAGCT	GTCTTCATTG	CGGTATGGT	GCTATTGTTG	3120
AACGCCTGGG	CAGCAGTACT	GGTGACATTA	GCGCTGGCTA	CATTAGTACT	GCAGCTGTTA	3180

GGTGTATGGC	CTTATTGGGC	GTGAAGCTAT	CTGCAATGCC	GGCCGTACTA	CTGGTGCTAG	3240
CCATTGGGAG	AGGAGTTCAC	TTCAGTGTGC	ATTTATGTTT	GGGTTTTGTA	ACATCAATCG	3300
GTTGCAAGCG	GCGCCGCGCG	TCACTAGCTC	TAGAATCAGT	TCTGGCGCCA	GTGGTGACACG	3360
GCGCTCTGGC	GGCCGCGCTG	GCTGCCTCGA	TGCTAGCTGC	AAGTGAATGT	GGCTTCGTTG	3420
CCAGACTGTT	CTTGAGGTTA	CTACTGGACA	TCGTGTTTCT	GGGACTCATC	GATGGGTTGC	3480
TGTTCTTCCC	TATTGTCCTT	TCGATATTGG	GACCGGCTGC	TGAGGTACGA	CCTATAGAGC	3540
ATCCAGAACG	CTTATCGACT	CCATCGCCAA	AATGTTGCGC	CATCCACCCT	CGCAAATCAA	3600
GTTCCAGCTC	AGGCGGTGGT	GATAAATCAA	GTCGAACCAG	TAAATCAGCA	CCAAGGCCTT	3660
GCGCACCATC	TCTCACGACC	ATTACTGAAG	AGCCTTCGAG	TTGGCACAGT	TCCGCCCCACT	3720
CCGTACAATC	TTCTATGCAG	TCGATAGTGG	TCCAGCCGGA	GGTGGTGGTC	GAAACTACCA	3780
CGTATAATGG	CAGCGATTCT	GCTTCAGGAC	GGTCGACGCC	TACAAAGTCT	TCACACGGTG	3840
GTGCTATCAC	AACTACTAAG	GTGACCGCCA	CGGCAAATAT	AAAGGTAGAA	GTGGTGACAC	3900
CGAGTGACAG	GAAATCGCGA	CGTTCCTATC	ATTACTATGA	TCGTCTGAAGG	GATCGCGATG	3960
AAGATAGGGA	TCGAGACCGT	GAAAGGGACA	GAGATCGCGA	CAGGGATCGG	GATAGGGATC	4020
GTGACCGGGA	CAGGGATAGG	GATAGAGAAC	GATCGAGAGA	ACGAGACAGG	CGAGACCGAT	4080
ATAGAGACGA	AAGGGACCAC	CGAGCTTCGC	CGAGAGAAAA	ACGGCAGAGA	TTCTGGACAT	4140
GAAAGTGATT	CATCACGTCA	TTAAGGATGA	AGTACATTGC	CAACTTGCCA	GAAACGCTCG	4200
TACAGTCGCG	GTATCTGAAC	ATATACCGGT	TGCGTTATTG	AATAACTTGT	AAATGATCTC	4260
TTTGATTTCG	CTTAAACATA	TTTTAGTTCA	CATCCTGCAA	CATCTTAATA	CGGTTAGGGT	4320
TAATTTTAAG	TCCATAATAG	TCGTATGTGG	TTGGTCCTTG	CGTTAAGTGC	ATTAGTTTTT	4380
TCCCATCACT	GGGTCCGTGG	CTTTTAATTT	GGTTTAACGG	GGGGGGACCT	TTTTTTTTTT	4440
TTTTTTTG						4448

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Val	Ala	Pro	Asp	Ser	Glu	Ala	Pro	Ser	Asn	Pro	Arg	Ile	Thr	Ala	1	5	10	15
Ala	His	Glu	Ser	Pro	Cys	Ala	Thr	Glu	Ala	Arg	His	Ser	Ala	Asp	Leu	20	25	30	
Tyr	Ile	Arg	Thr	Ser	Trp	Val	Asp	Ala	Ala	Leu	Ala	Leu	Ser	Glu	Leu	35	40	45	
Glu	Lys	Gly	Asn	Ile	Glu	Gly	Gly	Arg	Thr	Ser	Leu	Trp	Ile	Arg	Ala	50	55	60	
Trp	Leu	Gln	Glu	Gln	Leu	Phe	Ile	Leu	Gly	Cys	Phe	Leu	Gln	Gly	Asp	65	70	75	80
Ala	Gly	Lys	Val	Leu	Phe	Val	Ala	Ile	Leu	Val	Leu	Ser	Thr	Phe	Cys	85	90	95	
Val	Gly	Leu	Lys	Ser	Ala	Gln	Ile	His	Thr	Arg	Val	Asp	Gln	Leu	Trp	100	105	110	
Val	Gln	Glu	Gly	Gly	Arg	Leu	Glu	Ala	Glu	Leu	Lys	Tyr	Thr	Ala	Gln	115	120	125	
Ala	Leu	Gly	Glu	Ala	Asp	Ser	Ser	Thr	His	Gln	Leu	Val	Ile	Gln	Thr	130	135	140	
Ala	Lys	Asp	Pro	Asp	Val	Ser	Leu	Leu	His	Pro	Gly	Ala	Leu	Leu	Glu	145	150	155	160
His	Leu	Lys	Val	Val	His	Ala	Ala	Thr	Arg	Val	Thr	Val	His	Met	Tyr	165	170	175	
Asp	Ile	Glu	Trp	Arg	Leu	Lys	Asp	Leu	Cys	Tyr	Ser	Pro	Ser	Ile	Pro	180	185	190	
Asp	Phe	Glu	Gly	Tyr	His	His	Ile	Glu	Ser	Ile	Ile	Asp	Asn	Val	Ile	195	200	205	
Pro	Cys	Ala	Ile	Ile	Thr	Pro	Leu	Asp	Cys	Phe	Trp	Glu	Gly	Ser	Lys	210	215	220	
Leu	Leu	Gly	Pro	Asp	Tyr	Pro	Ile	Tyr	Val	Pro	His	Leu	Lys	His	Lys	225	230	235	240
Leu	Gln	Trp	Thr	His	Leu	Asn	Pro	Leu	Glu	Val	Val	Glu	Glu	Val	Lys	245	250	255	
Lys	Leu	Lys	Phe	Gln	Phe	Pro	Leu	Ser	Thr	Ile	Glu	Ala	Tyr	Met	Lys	260	265	270	
Arg	Ala	Gly	Ile	Thr	Ser	Ala	Tyr	Met	Lys	Lys	Pro	Cys	Leu	Asp	Pro	275	280	285	
Thr	Asp	Pro	His	Cys	Pro	Ala	Thr	Ala	Pro	Asn	Lys	Lys	Ser	Gly	His	290	295	300	
Ile	Pro	Asp	Val	Ala	Ala	Glu	Leu	Ser	His	Gly	Cys	Tyr	Gly	Phe	Ala				

305					310						315				320
Ala	Ala	Tyr	Met	His	Trp	Pro	Glu	Gln	Leu	Ile	Val	Gly	Gly	Ala	Thr
				325					330					335	
Arg	Asn	Ser	Thr	Ser	Ala	Leu	Arg	Lys	Ala	Arg	Xaa	Leu	Gln	Thr	Val
			340					345					350		
Val	Gln	Leu	Met	Gly	Glu	Arg	Glu	Met	Tyr	Glu	Tyr	Trp	Ala	Asp	His
		355					360					365			
Tyr	Lys	Val	His	Gln	Ile	Gly	Trp	Asn	Gln	Glu	Lys	Ala	Ala	Ala	Val
	370					375					380				
Leu	Asp	Ala	Trp	Gln	Arg	Lys	Phe	Ala	Ala	Glu	Val	Arg	Lys	Ile	Thr
385					390					395					400
Thr	Ser	Gly	Ser	Val	Ser	Ser	Ala	Tyr	Ser	Phe	Tyr	Pro	Phe	Ser	Thr
				405					410						415
Ser	Thr	Leu	Asn	Asp	Ile	Leu	Gly	Lys	Phe	Ser	Glu	Val	Ser	Leu	Lys
			420					425					430		
Asn	Ile	Ile	Leu	Gly	Tyr	Met	Phe	Met	Leu	Ile	Tyr	Val	Ala	Val	Thr
		435					440					445			
Leu	Ile	Gln	Trp	Arg	Asp	Pro	Ile	Arg	Ser	Gln	Ala	Gly	Val	Gly	Ile
	450					455					460				
Ala	Gly	Val	Leu	Leu	Leu	Ser	Ile	Thr	Val	Ala	Ala	Gly	Leu	Gly	Phe
465					470					475					480
Cys	Ala	Leu	Leu	Gly	Ile	Pro	Phe	Asn	Ala	Ser	Ser	Thr	Gln	Ile	Val
				485				490						495	
Pro	Phe	Leu	Ala	Leu	Gly	Leu	Gly	Val	Gln	Asp	Met	Phe	Leu	Leu	Thr
			500					505					510		
His	Thr	Tyr	Val	Glu	Gln	Ala	Gly	Asp	Val	Pro	Arg	Glu	Glu	Arg	Thr
		515					520					525			
Gly	Leu	Val	Leu	Lys	Lys	Ser	Gly	Leu	Ser	Val	Leu	Leu	Ala	Ser	Leu
	530					535					540				
Cys	Asn	Val	Met	Ala	Phe	Leu	Ala	Ala	Ala	Leu	Leu	Pro	Ile	Pro	Ala
545					550					555					560
Phe	Arg	Val	Phe	Cys	Leu	Gln	Ala	Ala	Ile	Leu	Leu	Leu	Phe	Asn	Leu
				565					570					575	
Gly	Ser	Ile	Leu	Leu	Val	Phe	Pro	Ala	Met	Ile	Ser	Leu	Asp	Leu	Arg
			580					585					590		
Arg	Arg	Ser	Ala	Ala	Arg	Ala	Asp	Leu	Leu	Cys	Cys	Leu	Met	Pro	Glu
		595					600					605			
Ser	Pro	Leu	Pro	Lys	Lys	Lys	Ile	Pro	Glu	Arg	Ala	Lys	Thr	Arg	Lys
	610					615					620				

Asn 625	Asp	Lys	Thr	His	Arg 630	Ile	Asp	Thr	Thr	Arg 635	Gln	Pro	Leu	Asp	Pro 640
Asp	Val	Ser	Glu	Asn 645	Val	Thr	Lys	Thr	Cys 650	Cys	Leu	Ser	Val	Ser 655	Leu
Thr	Lys	Trp	Ala 660	Lys	Asn	Gln	Tyr	Ala 665	Pro	Phe	Ile	Met	Arg 670	Pro	Ala
Val	Lys	Val	Thr	Ser	Met	Leu	Ala 680	Leu	Ile	Ala	Val	Ile 685	Leu	Thr	Ser
Val	Trp 690	Gly	Ala	Thr	Lys	Val 695	Lys	Asp	Gly	Leu	Asp 700	Leu	Thr	Asp	Ile
Val 705	Pro	Glu	Asn	Thr	Asp 710	Glu	His	Glu	Phe	Leu 715	Ser	Arg	Gln	Glu	Lys 720
Tyr	Phe	Gly	Phe	Tyr 725	Asn	Met	Tyr	Ala	Val 730	Thr	Gln	Gly	Asn	Phe 735	Glu
Tyr	Pro	Thr	Asn 740	Gln	Lys	Leu	Leu	Tyr 745	Glu	Tyr	His	Asp	Gln 750	Phe	Val
Arg	Ile	Pro 755	Asn	Ile	Ile	Lys	Asn 760	Asp	Asn	Gly	Gly	Leu	Thr	Lys	Phe
Trp 770	Leu	Ser	Leu	Phe	Arg	Asp 775	Trp	Leu	Leu	Asp	Leu	Gln	Val	Ala	Phe
Asp 785	Lys	Glu	Val	Ala	Ser 790	Gly	Cys	Ile	Thr	Gln 795	Glu	Tyr	Trp	Cys	Lys 800
Asn	Ala	Ser	Asp	Glu 805	Gly	Ile	Leu	Ala	Tyr 810	Lys	Leu	Met	Val	Gln 815	Thr
Gly	His	Val	Asp 820	Asn	Pro	Ile	Asp	Lys 825	Ser	Leu	Ile	Thr	Ala 830	Gly	His
Arg	Leu	Val 835	Asp	Lys	Asp	Gly	Ile 840	Ile	Asn	Pro	Lys	Ala 845	Phe	Tyr	Asn
Tyr 850	Leu	Ser	Ala	Trp	Ala	Thr	Asn 855	Asp	Ala	Leu	Ala 860	Tyr	Gly	Ala	Ser
Gln 865	Gly	Asn	Leu	Lys	Pro 870	Gln	Pro	Gln	Arg	Trp 875	Ile	His	Ser	Pro	Glu 880
Asp	Val	His	Leu	Glu 885	Ile	Lys	Lys	Ser	Ser 890	Pro	Leu	Ile	Tyr	Thr 895	Gln
Leu	Pro	Phe	Tyr 900	Leu	Ser	Gly	Leu	Ser 905	Asp	Thr	Xaa	Ser	Ile 910	Lys	Thr
Leu	Ile	Arg 915	Ser	Val	Arg	Asp	Leu 920	Cys	Leu	Lys	Tyr	Glu 925	Ala	Lys	Gly
Leu	Pro	Asn	Phe	Pro	Ser	Gly	Ile	Pro	Phe	Leu	Phe	Trp	Glu	Gln	Tyr

930					935					940				
Leu Tyr Leu Arg Thr Ser	Leu Leu Leu Ala Leu Ala Cys Ala Leu Ala	945	950	955	960									
Ala Val Phe Ile Ala Val Met Val Leu Leu Leu Asn Ala Trp Ala Ala			965	970	975									
Val Leu Val Thr Leu Ala Leu Ala Thr Leu Val Leu Gln Leu Leu Gly			980	985	990									
Val Met Ala Leu Leu Gly Val Lys Leu Ser Ala Met Pro Ala Val Leu			995	1000	1005									
Leu Val Leu Ala Ile Gly Arg Gly Val His Phe Thr Val His Leu Cys			1010	1015	1020									
Leu Gly Phe Val Thr Ser Ile Gly Cys Lys Arg Arg Arg Ala Ser Leu			1025	1030	1035							1040		
Ala Leu Glu Ser Val Leu Ala Pro Val Val His Gly Ala Leu Ala Ala			1045	1050	1055									
Ala Leu Ala Ala Ser Met Leu Ala Ala Ser Glu Cys Gly Phe Val Ala			1060	1065	1070									
Arg Leu Phe Leu Arg Leu Leu Leu Asp Ile Val Phe Leu Gly Leu Ile			1075	1080	1085									
Asp Gly Leu Leu Phe Phe Pro Ile Val Leu Ser Ile Leu Gly Pro Ala			1090	1095	1100									
Ala Glu Val Arg Pro Ile Glu His Pro Glu Arg Leu Ser Thr Pro Ser			1105	1110	1115							1120		
Pro Lys Cys Ser Pro Ile His Pro Arg Lys Ser Ser Ser Ser Ser Gly			1125	1130	1135									
Gly Gly Asp Lys Ser Ser Arg Thr Ser Lys Ser Ala Pro Arg Pro Cys			1140	1145	1150									
Ala Pro Ser Leu Thr Thr Ile Thr Glu Glu Pro Ser Ser Trp His Ser			1155	1160	1165									
Ser Ala His Ser Val Gln Ser Ser Met Gln Ser Ile Val Val Gln Pro			1170	1175	1180									
Glu Val Val Val Glu Thr Thr Thr Tyr Asn Gly Ser Asp Ser Ala Ser			1185	1190	1195							1200		
Gly Arg Ser Thr Pro Thr Lys Ser Ser His Gly Gly Ala Ile Thr Thr			1205	1210	1215									
Thr Lys Val Thr Ala Thr Ala Asn Ile Lys Val Glu Val Val Thr Pro			1220	1225	1230									
Ser Asp Arg Lys Ser Arg Arg Ser Tyr His Tyr Tyr Asp Arg Arg Arg			1235	1240	1245									

Asp Arg Asp Glu Asp Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp Arg
 1250 1255 1260

Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg
 1265 1270 1275 1280

Glu Arg Ser Arg Glu Arg Asp Arg Arg Asp Arg Tyr Arg Asp Glu Arg
 1285 1290 1295

Asp His Arg Ala Ser Pro Arg Glu Lys Arg Gln Arg Phe Trp Thr
 1300 1305 1310

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAAACAAGA GAGCGAGTGA GAGTAGGGAG AGCGTCTGTG TTGTGTGTTG AGTGTCGCCC	60
ACGCACACAG GCGCAAAACA GTGCACACAG ACGCCCGCTG GGCAAGAGAG AGTGAGAGAG	120
AGAAACAGCG GCGCGCGCTC GCCTAATGAA GTTGTTGGCC TGGCTGGCGT GCCGCATCCA	180
CGAGATACAG ATACATCTCT CATGGACCGC GACAGCCTCC CACGCGTTCC GGACACACAC	240
GGCGATGTGG TCGATGAGAA ATTATTCTCG GATCTTTACA TACGCACCAG CTGGGTGGAC	300
GCCCAAGTGG CGCTCGATCA GATAGATAAG GGCAAAGCGC GTGGCAGCCG CACGGCGATC	360
TATCTGCGAT CAGTATTCCA GTCCACCTC GAAACCCTCG GCAGCTCCGT GCAAAAGCAC	420
GCGGGCAAGG TGCTATTCGT GGCTATCCTG GTGCTGAGCA CCTTCTGCGT CGGCCTGAAG	480
AGCGCCCAGA TCCACTCCAA GGTGCACCAG CTGTGGATCC AGGAGGGCGG CCGGCTGGAG	540
GCGGAACTGG CCTACACACA GAAGACGATC GGCGAGGACG AGTCGGCCAC GCATCAGCTG	600
CTCATTCAGA CGACCCACGA CCCGAACGCC TCCGTCCTGC ATCCGCAGGC GCTGCTTGCC	660
CACCTGGAGG TCCTGGTCAA GGCCACCGCC GTCAAGGTGC ACCTCTACGA CACCGAATGG	720
GGGCTGCGCG ACATGTGCAA CATGCCGAGC ACGCCCTCCT TCGAGGGCAT CTA CTACATC	780
GAGCAGATCC TGCGCCACCT CATTCCGTGC TCGATCATCA CGCCGCTGGA CTGTTTCTGG	840
GAGGGAAGCC AGCTGTTGGG TCCGGAATCA GCGGTCGTTA TACCAGGCCT CAACCAACGA	900
CTCCTGTGGA CCACCCTGAA TCCCGCCTCT GTGATGCAGT ATATGAAACA AAAGATGTCC	960

GAGGAAAAGA	TCAGCTTCGA	CTTCGAGACC	GTGGAGCAGT	ACATGAAGCG	TGCGGCCATT	1020
GGCAGTGGCT	ACATGGAGAA	GCCCTGCCTG	AACCCACTGA	ATCCCAATTG	CCCGGACACG	1080
GCACCGAACA	AGAACAGCAC	CCAGCCGCCG	GATGTGGGAG	CCATCCTGTC	CGGAGGCTGC	1140
TACGGTTATG	CCGCGAAGCA	CATGCACTGG	CCGGAGGAGC	TGATTGTGGG	CGGACGGAAG	1200
AGGAACCGCA	GCGGACACTT	GAGGAAGGCC	CAGGCCCTGC	AGTCGGTGGT	GCAGCTGATG	1260
ACCGAGAAGG	AAATGTACGA	CCAGTGGCAG	GACAACTACA	AGGTGCACCA	TCTTGGATGG	1320
ACGCAGGAGA	AGGCAGCGGA	GGTTTTGAAC	GCCTGGCAGC	GCAACTTTTC	GCGGGAGGTG	1380
GAACAGCTGC	TACGTAAACA	GTCGAGAATT	GCCACCAACT	ACGATATCTA	CGTGTTTCAGC	1440
TCGGCTGCAC	TGGATGACAT	CCTGGCCAAG	TTCTCCCATC	CCAGCGCCTT	GTCCATTGTC	1500
ATCGGCGTGG	CCGTCACCGT	TTTGTATGCC	TTTTGCACGC	TCCTCCGCTG	GAGGGACCCC	1560
GTCCGTGGCC	AGAGCAGTGT	GGGCGTGGCC	GGAGTTCTGC	TCATGTGCTT	CAGTACCGCC	1620
GCCGGATTGG	GATTGTCAGC	CCTGCTCGGT	ATCGTTTTCA	ATGCGCTGAC	CGCTGCCTAT	1680
GCGGAGAGCA	ATCGGCGGGA	GCAGACCAAG	CTGATTCTCA	AGAACGCCAG	CACCCAGGTG	1740
GTTCCGTTTT	TGGCCCTTGG	TCTGGGCGTC	GATCACATCT	TCATAGTGGG	ACCGAGCATC	1800
CTGTTTCAGTG	CCTGCAGCAC	CGCAGGATCC	TTCTTTGCGG	CCGCCTTTAT	TCCGGTGCCG	1860
GCTTTGAAGG	TATTCTGTCT	GCAGGCTGCC	ATCGTAATGT	GCTCCAATTT	GGCAGCGGCT	1920
CTATTGGTTT	TTCCGGCCAT	GATTTTCGTTG	GATCTACGGA	GACGTACCGC	CGGCAGGGCG	1980
GACATCTTCT	GCTGCTGTTT	TCCGGTGTGG	AAGGAACAGC	CGAAGGTGGC	ACCTCCGGTG	2040
CTGCCGCTGA	ACAACAACAA	CGGGCGCGGG	GCCCGGCATC	CGAAGAGCTG	CAACAACAAC	2100
AGGGTGCCGC	TGCCCCCCCA	GAATCCTCTG	CTGGAACAGA	GGGCAGACAT	CCCTGGGAGC	2160
AGTCACTCAC	TGGCGTCCTT	CTCCCTGGCA	ACCTTCGCCT	TTCAGCACTA	CACTCCCTTC	2220
CTCATGCGCA	GCTGGGTGAA	GTTCTTGACC	GTTATGGGTT	TCCTGGCGGC	CCTCATATCC	2280
AGCTTGATATG	CCTCCACGCG	CCTTCAGGAT	GGCCTGGACA	TTATTGATCT	GGTGCCCAAG	2340
GACAGCAACG	AGCACAAGTT	CCTGGATGCT	CAAACCTCGGC	TCTTTGGCTT	CTACAGCATG	2400
TATGCGGTTA	CCCAGGGCAA	CTTTGAATAT	CCCACCCAGC	AGCAGTTGCT	CAGGGACTAC	2460
CATGATTCCT	TTGTGCGGGT	GCCACATGTG	ATCAAGAATG	ATAACGGTGG	ACTGCCGGAC	2520
TTCTGGCTGC	TGCTCTTCAG	CGAGTGGCTG	GGTAATCTGC	AAAAGATATT	CGACGAGGAA	2580
TACCGCGACG	GACGGCTGAC	CAAGGAGTGC	TGGTTCCCAA	ACGCCAGCAG	CGATGCCATC	2640
CTGGCCTACA	AGCTAATCGT	GCAAACCGGC	CATGTGGACA	ACCCCGTGGA	CAAGGAACTG	2700

GTGCTCACCA	ATCGCCTGGT	CAACAGCGAT	GGCATCATCA	ACCAACGCGC	CTTCTACAAC	2760
TATCTGTCGG	CATGGGCCAC	CAACGACGTC	TTCGCCTACG	GAGCTTCTCA	GGGCAAATTG	2820
TATCCGGAAC	CGCGCCAGTA	TTTTACCAA	CCCAACGAGT	ACGATCTTAA	GATACCCAAG	2880
AGTCTGCCAT	TGGTCTACGC	TCAGATGCCC	TTTTACCTCC	ACGGACTAAC	AGATACCTCG	2940
CAGATCAAGA	CCCTGATAGG	TCATATTCGC	GACCTGAGCG	TCAAGTACGA	GGGCTTCGGC	3000
CTGCCCAACT	ATCCATCGGG	CATTCCCTTC	ATCTTCTGGG	AGCAGTACAT	GACCCTGCGC	3060
TCCTCACTGG	CCATGATCCT	GGCCTGCGTG	CTACTCGCCG	CCCTGGTGCT	GGTCTCCCTG	3120
CTCCTGCTCT	CCGTTTGGGC	CGCCGTTCCTC	GTGATCCTCA	GCGTTCTGGC	CTCGCTGGCC	3180
CAGATCTTTG	GGGCCATGAC	TCTGCTGGGC	ATCAAACCTCT	CGGCCATTCC	GGCAGTCATA	3240
CTCATCCTCA	GCGTGGGCAT	GATGCTGTGC	TTCAATGTGC	TGATATCACT	GGGCTTCATG	3300
ACATCCGTTG	GCAACCGACA	GCGCCGCGTC	CAGCTGAGCA	TGCAGATGTC	CCTGGGACCA	3360
CTTGTCACG	GCATGCTGAC	CTCCGGAGTG	GCCGTGTTCA	TGCTCTCCAC	GTCGCCCTTT	3420
GAGTTTGTGA	TCCGGCACTT	CTGCTGGCTT	CTGCTGGTGG	TCTTATGCGT	TGGCGCCTGC	3480
AACAGCCTTT	TGGTGTTCCC	CATCCTACTG	AGCATGGTGG	GACCGGAGGC	GGAGCTGGTG	3540
CCGCTGGAGC	ATCCAGACCG	CATATCCACG	CCCTCTCCGC	TGCCCCGTGCG	CAGCAGCAAG	3600
AGATCGGGCA	AATCCTATGT	GGTGCAGGGA	TCGCGATCCT	CGCGAGGCAG	CTGCCAGAAG	3660
TCGCATCACC	ACCACCACAA	AGACCTTAAT	GATCCATCGC	TGACGACGAT	CACCGAGGAG	3720
CCGCAGTCGT	GGAAGTCCAG	CAACTCGTCC	ATCCAGATGC	CCAATGATTG	GACCTACCAG	3780
CCGCGGGAAC	AGCGACCCGC	CTCCTACGCG	GCCCCGCCCC	CCGCCTATCA	CAAGGCCGCC	3840
GCCCAGCAGC	ACCACCAGCA	TCAGGGCCCC	CCCACAACGC	CCCCGCCTCC	CTTCCCAGC	3900
GCCTATCCGC	CGGAGCTGCA	GAGCATCGTG	GTGCAGCCGG	AGGTGACGGT	GGAGACGACG	3960
CACTCGGACA	GCAACACCAC	CAAGGTGACG	GCCACGGCCA	ACATCAAGGT	GGAGCTGGCC	4020
ATGCCCCGGCA	GGGCGGTGCG	CAGCTATAAC	TTTACGAGTT	AGCACTAGCA	CTAGTTCCTG	4080
TAGCTATTAG	GACGTATCTT	TAGACTCTAG	CCTAAGCCGT	AACCCTATTT	GTATCTGTAA	4140
AATCGATTTG	TCCAGCGGGT	CTGCTGAGGA	TTTCGTTCTC	ATGGATTCTC	ATGGATTCTC	4200
ATGGATGCTT	AAATGGCATG	GTAATTGGCA	AAATATCAAT	TTTTGTGTCT	CAAAAAGATG	4260
CATTAGCTTA	TGGTTTCAAG	ATACATTTTT	AAAGAGTCCG	CCAGATATTT	ATATAAAAAA	4320
AATCCAAAAT	CGACGTATCC	ATGAAAATTG	AAAAGCTAAG	CAGACCCGTA	TGTATGTATA	4380
TGTGTATGCA	TGTTAGTTAA	TTTCCCGAAG	TCCGGTATTT	ATAGCAGCTG	CCTT	4434

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asp	Arg	Asp	Ser	Leu	Pro	Arg	Val	Pro	Asp	Thr	His	Gly	Asp	Val
1				5					10					15	
Val	Asp	Glu	Lys	Leu	Phe	Ser	Asp	Leu	Tyr	Ile	Arg	Thr	Ser	Trp	Val
			20					25					30		
Asp	Ala	Gln	Val	Ala	Leu	Asp	Gln	Ile	Asp	Lys	Gly	Lys	Ala	Arg	Gly
		35					40					45			
Ser	Arg	Thr	Ala	Ile	Tyr	Leu	Arg	Ser	Val	Phe	Gln	Ser	His	Leu	Glu
	50					55					60				
Thr	Leu	Gly	Ser	Ser	Val	Gln	Lys	His	Ala	Gly	Lys	Val	Leu	Phe	Val
65					70					75					80
Ala	Ile	Leu	Val	Leu	Ser	Thr	Phe	Cys	Val	Gly	Leu	Lys	Ser	Ala	Gln
				85					90					95	
Ile	His	Ser	Lys	Val	His	Gln	Leu	Trp	Ile	Gln	Glu	Gly	Gly	Arg	Leu
			100					105					110		
Glu	Ala	Glu	Leu	Ala	Tyr	Thr	Gln	Lys	Thr	Ile	Gly	Glu	Asp	Glu	Ser
		115					120					125			
Ala	Thr	His	Gln	Leu	Leu	Ile	Gln	Thr	Thr	His	Asp	Pro	Asn	Ala	Ser
	130					135					140				
Val	Leu	His	Pro	Gln	Ala	Leu	Leu	Ala	His	Leu	Glu	Val	Leu	Val	Lys
145					150					155					160
Ala	Thr	Ala	Val	Lys	Val	His	Leu	Tyr	Asp	Thr	Glu	Trp	Gly	Leu	Arg
				165					170					175	
Asp	Met	Cys	Asn	Met	Pro	Ser	Thr	Pro	Ser	Phe	Glu	Gly	Ile	Tyr	Tyr
			180					185					190		
Ile	Glu	Gln	Ile	Leu	Arg	His	Leu	Ile	Pro	Cys	Ser	Ile	Ile	Thr	Pro
		195					200					205			
Leu	Asp	Cys	Phe	Trp	Glu	Gly	Ser	Gln	Leu	Leu	Gly	Pro	Glu	Ser	Ala
	210					215					220				
Val	Val	Ile	Pro	Gly	Leu	Asn	Gln	Arg	Leu	Leu	Trp	Thr	Thr	Leu	Asn
225					230					235					240

Pro	Ala	Ser	Val	Met 245	Gln	Tyr	Met	Lys	Gln 250	Lys	Met	Ser	Glu	Glu 255	Lys	
Ile	Ser	Phe	Asp 260	Phe	Glu	Thr	Val	Glu 265	Gln	Tyr	Met	Lys	Arg 270	Ala	Ala	
Ile	Gly	Ser 275	Gly	Tyr	Met	Glu	Lys 280	Pro	Cys	Leu	Asn	Pro 285	Leu	Asn	Pro	
Asn	Cys 290	Pro	Asp	Thr	Ala	Pro 295	Asn	Lys	Asn	Ser	Thr 300	Gln	Pro	Pro	Asp	
Val 305	Gly	Ala	Ile	Leu	Ser 310	Gly	Gly	Cys	Tyr	Gly 315	Tyr	Ala	Ala	Lys	His 320	
Met	His	Trp	Pro	Glu 325	Glu	Leu	Ile	Val	Gly 330	Gly	Arg	Lys	Arg	Asn 335	Arg	
Ser	Gly	His	Leu 340	Arg	Lys	Ala	Gln	Ala 345	Leu	Gln	Ser	Val	Val 350	Gln	Leu	
Met	Thr	Glu 355	Lys	Glu	Met	Tyr	Asp 360	Gln	Trp	Gln	Asp	Asn 365	Tyr	Lys	Val	
His	His 370	Leu	Gly	Trp	Thr	Gln	Glu	Lys	Ala	Ala	Glu 380	Val	Leu	Asn	Ala	
Trp 385	Gln	Arg	Asn	Phe	Ser 390	Arg	Glu	Val	Glu	Gln 395	Leu	Leu	Arg	Lys	Gln 400	
Ser	Arg	Ile	Ala	Thr 405	Asn	Tyr	Asp	Ile	Tyr 410	Val	Phe	Ser	Ser	Ala 415	Ala	
Leu	Asp	Asp	Ile 420	Leu	Ala	Lys	Phe	Ser 425	His	Pro	Ser	Ala	Leu 430	Ser	Ile	
Val	Ile	Gly 435	Val	Ala	Val	Thr	Val 440	Leu	Tyr	Ala	Phe	Cys 445	Thr	Leu	Leu	
Arg 450	Trp	Arg	Asp	Pro	Val	Arg 455	Gly	Gln	Ser	Ser	Val 460	Gly	Val	Ala	Gly	
Val 465	Leu	Leu	Met	Cys	Phe 470	Ser	Thr	Ala	Ala	Gly 475	Leu	Gly	Leu	Ser	Ala 480	
Leu	Leu	Gly	Ile	Val 485	Phe	Asn	Ala	Leu	Thr 490	Ala	Ala	Tyr	Ala	Glu 495	Ser	
Asn	Arg	Arg	Glu 500	Gln	Thr	Lys	Leu	Ile 505	Leu	Lys	Asn	Ala	Ser 510	Thr	Gln	
Val	Val	Pro 515	Phe	Leu	Ala	Leu	Gly 520	Leu	Gly	Val	Asp	His 525	Ile	Phe	Ile	
Val 530	Gly	Pro	Ser	Ile	Leu	Phe 535	Ser	Ala	Cys	Ser	Thr 540	Ala	Gly	Ser	Phe	
Phe	Ala	Ala	Ala	Phe	Ile	Pro	Val	Pro	Ala	Leu	Lys	Val	Phe	Cys	Leu	

545		550		555		560
Gln Ala Ala Ile Val Met Cys Ser Asn Leu Ala Ala Ala Leu Leu Val						
		565		570		575
Phe Pro Ala Met Ile Ser Leu Asp Leu Arg Arg Arg Thr Ala Gly Arg		580		585		590
Ala Asp Ile Phe Cys Cys Cys Phe Pro Val Trp Lys Glu Gln Pro Lys		595		600		605
Val Ala Pro Pro Val Leu Pro Leu Asn Asn Asn Asn Gly Arg Gly Ala		610		615		620
Arg His Pro Lys Ser Cys Asn Asn Asn Arg Val Pro Leu Pro Ala Gln		625		630		635
						640
Asn Pro Leu Leu Glu Gln Arg Ala Asp Ile Pro Gly Ser Ser His Ser		645		650		655
Leu Ala Ser Phe Ser Leu Ala Thr Phe Ala Phe Gln His Tyr Thr Pro		660		665		670
Phe Leu Met Arg Ser Trp Val Lys Phe Leu Thr Val Met Gly Phe Leu		675		680		685
Ala Ala Leu Ile Ser Ser Leu Tyr Ala Ser Thr Arg Leu Gln Asp Gly		690		695		700
Leu Asp Ile Ile Asp Leu Val Pro Lys Asp Ser Asn Glu His Lys Phe		705		710		715
						720
Leu Asp Ala Gln Thr Arg Leu Phe Gly Phe Tyr Ser Met Tyr Ala Val		725		730		735
Thr Gln Gly Asn Phe Glu Tyr Pro Thr Gln Gln Gln Leu Leu Arg Asp		740		745		750
Tyr His Asp Ser Phe Val Arg Val Pro His Val Ile Lys Asn Asp Asn		755		760		765
Gly Gly Leu Pro Asp Phe Trp Leu Leu Leu Phe Ser Glu Trp Leu Gly		770		775		780
Asn Leu Gln Lys Ile Phe Asp Glu Glu Tyr Arg Asp Gly Arg Leu Thr		785		790		795
						800
Lys Glu Cys Trp Phe Pro Asn Ala Ser Ser Asp Ala Ile Leu Ala Tyr		805		810		815
Lys Leu Ile Val Gln Thr Gly His Val Asp Asn Pro Val Asp Lys Glu		820		825		830
Leu Val Leu Thr Asn Arg Leu Val Asn Ser Asp Gly Ile Ile Asn Gln		835		840		845
Arg Ala Phe Tyr Asn Tyr Leu Ser Ala Trp Ala Thr Asn Asp Val Phe		850		855		860

Ala	Tyr	Gly	Ala	Ser	Gln	Gly	Lys	Leu	Tyr	Pro	Glu	Pro	Arg	Gln	Tyr	865	870	875	880
Phe	His	Gln	Pro	Asn	Glu	Tyr	Asp	Leu	Lys	Ile	Pro	Lys	Ser	Leu	Pro	885	890	895	
Leu	Val	Tyr	Ala	Gln	Met	Pro	Phe	Tyr	Leu	His	Gly	Leu	Thr	Asp	Thr	900	905	910	
Ser	Gln	Ile	Lys	Thr	Leu	Ile	Gly	His	Ile	Arg	Asp	Leu	Ser	Val	Lys	915	920	925	
Tyr	Glu	Gly	Phe	Gly	Leu	Pro	Asn	Tyr	Pro	Ser	Gly	Ile	Pro	Phe	Ile	930	935	940	
Phe	Trp	Glu	Gln	Tyr	Met	Thr	Leu	Arg	Ser	Ser	Leu	Ala	Met	Ile	Leu	945	950	955	960
Ala	Cys	Val	Leu	Leu	Ala	Ala	Leu	Val	Leu	Val	Ser	Leu	Leu	Leu	Leu	965	970	975	
Ser	Val	Trp	Ala	Ala	Val	Leu	Val	Ile	Leu	Ser	Val	Leu	Ala	Ser	Leu	980	985	990	
Ala	Gln	Ile	Phe	Gly	Ala	Met	Thr	Leu	Leu	Gly	Ile	Lys	Leu	Ser	Ala	995	1000	1005	
Ile	Pro	Ala	Val	Ile	Leu	Ile	Leu	Ser	Val	Gly	Met	Met	Leu	Cys	Phe	1010	1015	1020	
Asn	Val	Leu	Ile	Ser	Leu	Gly	Phe	Met	Thr	Ser	Val	Gly	Asn	Arg	Gln	1025	1030	1035	1040
Arg	Arg	Val	Gln	Leu	Ser	Met	Gln	Met	Ser	Leu	Gly	Pro	Leu	Val	His	1045	1050	1055	
Gly	Met	Leu	Thr	Ser	Gly	Val	Ala	Val	Phe	Met	Leu	Ser	Thr	Ser	Pro	1060	1065	1070	
Phe	Glu	Phe	Val	Ile	Arg	His	Phe	Cys	Trp	Leu	Leu	Leu	Val	Val	Leu	1075	1080	1085	
Cys	Val	Gly	Ala	Cys	Asn	Ser	Leu	Leu	Val	Phe	Pro	Ile	Leu	Leu	Ser	1090	1095	1100	
Met	Val	Gly	Pro	Glu	Ala	Glu	Leu	Val	Pro	Leu	Glu	His	Pro	Asp	Arg	1105	1110	1115	1120
Ile	Ser	Thr	Pro	Ser	Pro	Leu	Pro	Val	Arg	Ser	Ser	Lys	Arg	Ser	Gly	1125	1130	1135	
Lys	Ser	Tyr	Val	Val	Gln	Gly	Ser	Arg	Ser	Ser	Arg	Gly	Ser	Cys	Gln	1140	1145	1150	
Lys	Ser	His	His	His	His	His	Lys	Asp	Leu	Asn	Asp	Pro	Ser	Leu	Thr	1155	1160	1165	
Thr	Ile	Thr	Glu	Glu	Pro	Gln	Ser	Trp	Lys	Ser	Ser	Asn	Ser	Ser	Ile				

1170	1175	1180
Gln Met Pro Asn Asp Trp Thr Tyr Gln Pro Arg Glu Gln Arg Pro Ala 1185	1190	1195 1200
Ser Tyr Ala Ala Pro Pro Pro Ala Tyr His Lys Ala Ala Ala Gln Gln 1205	1210	1215
His His Gln His Gln Gly Pro Pro Thr Thr Pro Pro Pro Pro Phe Pro 1220	1225	1230
Thr Ala Tyr Pro Pro Glu Leu Gln Ser Ile Val Val Gln Pro Glu Val 1235	1240	1245
Thr Val Glu Thr Thr His Ser Asp Ser Asn Thr Thr Lys Val Thr Ala 1250	1255	1260
Thr Ala Asn Ile Lys Val Glu Leu Ala Met Pro Gly Arg Ala Val Arg 1265	1270	1275 1280
Ser Tyr Asn Phe Thr Ser 1285		

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGGTCCATC AGCTTTGGAT ACAGGAAGGT GGTTCGCTCG AGCATGAGCT AGCCTACACG	60
CAGAAATCGC TCGGCGAGAT GGACTCCTCC ACGCACCAGC TGCTAATCCA AACCCCAAAG	120
ATATGGACGC CTCGATACTG CACCCGAACG CGCTACTGAC GCACCTGGAC GTGGTGAAGA	180
AAGCGATCTC GGTGACGGTG CACATGTACG ACATCACGTG GAGCTCAAGG ACATGTGCTA	240
CTCGCCCAGC ATACCGAGTT CGATACGCAC TTTATCGAGC AGATCTTCGA GAACATCATA	300
CCGTGCGCGA TCATCACGCC GCTGGATTGC TTTTGGGAGG GA	342

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys	Val	His	Gln	Leu	Trp	Ile	Gln	Glu	Gly	Gly	Ser	Leu	Glu	His	Glu
1				5					10					15	
Leu	Ala	Tyr	Thr	Gln	Lys	Ser	Leu	Gly	Glu	Met	Asp	Ser	Ser	Thr	His
			20					25					30		
Gln	Leu	Leu	Ile	Gln	Thr	Pro	Lys	Asp	Met	Asp	Ala	Ser	Ile	Leu	His
		35					40					45			
Pro	Asn	Ala	Leu	Leu	Thr	His	Leu	Asp	Val	Val	Lys	Lys	Ala	Ile	Ser
	50					55					60				
Val	Thr	Val	His	Met	Tyr	Asp	Ile	Thr	Trp	Xaa	Leu	Lys	Asp	Met	Cys
65					70					75					80
Tyr	Ser	Pro	Ser	Ile	Pro	Xaa	Phe	Asp	Thr	His	Phe	Ile	Glu	Gln	Ile
				85					90					95	
Phe	Glu	Asn	Ile	Ile	Pro	Cys	Ala	Ile	Ile	Thr	Pro	Leu	Asp	Cys	Phe
			100					105					110		
Trp	Glu	Gly													

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGATGTTAAT ATTCTCATCG

20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1356 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ala	Ser	Ala	Gly	Asn	Ala	Arg	Arg	Gly	Pro	Gly	Gln	Ala	Gly	Arg	
1				5					10					15		
Arg	Arg	Glu	Ala	Gln	Thr	Asp	Arg	Gly	Thr	Ala	Pro	Arg	Arg	Ala	Gly	
			20					25					30			
Pro	Gly	Leu	Ser	Ala	Pro	Ala	Gln	Leu	Leu	Arg	Arg	Ala	Phe	Ala	Leu	
		35					40					45				
Glu	Gln	Ile	Ser	Lys	Gly	Lys	Ala	Thr	Gly	Arg	Lys	Ala	Pro	Leu	Trp	
	50					55					60					
Leu	Arg	Ala	Lys	Phe	Gln	Arg	Leu	Leu	Phe	Lys	Leu	Gly	Cys	Tyr	Ile	
65					70					75					80	
Gln	Lys	Asn	Cys	Gly	Lys	Phe	Leu	Val	Val	Gly	Leu	Leu	Ile	Phe	Gly	
				85					90					95		
Ala	Phe	Ala	Val	Gly	Leu	Lys	Ala	Ala	Asn	Leu	Glu	Thr	Asn	Val	Glu	
			100					105					110			
Glu	Leu	Trp	Val	Glu	Val	Gly	Gly	Arg	Val	Ser	Arg	Glu	Leu	Asn	Tyr	
		115					120					125				
Thr	Arg	Gln	Lys	Ile	Gly	Glu	Glu	Ala	Met	Phe	Asn	Pro	Gln	Leu	Met	
	130					135					140					
Ile	Gln	Thr	Pro	Lys	Glu	Glu	Gly	Ala	Asn	Val	Leu	Thr	Thr	Glu	Ala	
145					150					155					160	
Leu	Leu	Gln	His	Leu	Asp	Ser	Ala	Leu	Gln	Ala	Ser	Arg	Val	His	Val	
				165					170					175		
Tyr	Met	Tyr	Asn	Arg	Gln	Trp	Lys	Leu	Glu	His	Leu	Cys	Tyr	Lys	Ser	
			180					185					190			
Gly	Glu	Leu	Ile	Thr	Glu	Thr	Gly	Tyr	Met	Asp	Gln	Ile	Ile	Glu	Tyr	
		195					200					205				
Leu	Tyr	Pro	Cys	Leu	Ile	Ile	Thr	Pro	Leu	Asp	Cys	Phe	Trp	Glu	Gly	
	210					215					220					
Ala	Lys	Leu	Gln	Ser	Gly	Thr	Ala	Tyr	Leu	Leu	Gly	Lys	Pro	Pro	Leu	
225					230					235					240	
Arg	Trp	Thr	Asn	Phe	Asp	Pro	Leu	Glu	Phe	Leu	Glu	Glu	Leu	Lys	Lys	
				245					250					255		
Ile	Asn	Tyr	Gln	Val	Asp	Ser	Trp	Glu	Glu	Met	Leu	Asn	Lys	Ala	Glu	
			260					265					270			
Val	Gly	His	Gly	Tyr	Met	Asp	Arg	Pro	Cys	Leu	Asn	Pro	Ala	Asp	Pro	
		275					280					285				
Asp	Cys	Pro	Ala	Thr	Ala	Pro	Asn	Lys	Asn	Ser	Thr	Lys	Pro	Leu	Asp	
	290					295					300					
Val	Ala	Leu	Val	Leu	Asn	Gly	Gly	Cys	Gln	Gly	Leu	Ser	Arg	Lys	Tyr	

305					310					315				320	
Met	His	Trp	Gln	Glu	Glu	Leu	Ile	Val	Gly	Gly	Thr	Val	Lys	Asn	Ala
				325					330					335	
Thr	Gly	Lys	Leu	Val	Ser	Ala	His	Ala	Leu	Gln	Thr	Met	Phe	Gln	Leu
			340					345					350		
Met	Thr	Pro	Lys	Gln	Met	Tyr	Glu	His	Phe	Arg	Gly	Tyr	Asp	Tyr	Val
		355					360					365			
Ser	His	Ile	Asn	Trp	Asn	Glu	Asp	Arg	Ala	Ala	Ala	Ile	Leu	Glu	Ala
	370					375					380				
Trp	Gln	Arg	Thr	Tyr	Val	Glu	Val	Val	His	Gln	Ser	Val	Ala	Pro	Asn
385					390					395					400
Ser	Thr	Gln	Lys	Val	Leu	Pro	Phe	Thr	Thr	Thr	Thr	Leu	Asp	Asp	Ile
				405					410					415	
Leu	Lys	Ser	Phe	Ser	Asp	Val	Ser	Val	Ile	Arg	Val	Ala	Ser	Gly	Tyr
			420					425					430		
Leu	Leu	Met	Leu	Ala	Tyr	Ala	Cys	Leu	Thr	Met	Leu	Arg	Trp	Asp	Cys
		435					440					445			
Ser	Lys	Ser	Gln	Gly	Ala	Val	Gly	Leu	Ala	Gly	Val	Leu	Leu	Val	Ala
	450					455					460				
Leu	Ser	Val	Ala	Ala	Gly	Leu	Gly	Leu	Cys	Ser	Leu	Ile	Gly	Ile	Ser
465					470					475					480
Phe	Asn	Ala	Ala	Thr	Thr	Gln	Val	Leu	Pro	Phe	Leu	Ala	Leu	Gly	Val
				485					490					495	
Gly	Val	Asp	Asp	Val	Phe	Leu	Leu	Ala	His	Ala	Phe	Ser	Glu	Thr	Gly
			500					505					510		
Gln	Asn	Lys	Arg	Ile	Pro	Phe	Glu	Asp	Arg	Thr	Gly	Glu	Cys	Leu	Lys
		515					520					525			
Arg	Thr	Gly	Ala	Ser	Val	Ala	Leu	Thr	Ser	Ile	Ser	Asn	Val	Thr	Ala
	530					535					540				
Phe	Phe	Met	Ala	Ala	Leu	Ile	Pro	Ile	Pro	Ala	Leu	Arg	Ala	Phe	Ser
545					550					555					560
Leu	Gln	Ala	Ala	Val	Val	Val	Val	Phe	Asn	Phe	Ala	Met	Val	Leu	Leu
				565					570					575	
Ile	Phe	Pro	Ala	Ile	Leu	Ser	Met	Asp	Leu	Tyr	Arg	Arg	Glu	Asp	Arg
			580					585					590		
Arg	Leu	Asp	Ile	Phe	Cys	Cys	Leu	Thr	Ser	Pro	Cys	Val	Ser	Arg	Val
		595					600					605			
Ile	Gln	Val	Glu	Pro	Gln	Ala	Tyr	Thr	Glu	Pro	His	Ser	Asn	Thr	Arg
	610					615					620				

Tyr 625	Ser	Pro	Pro	Pro	Pro 630	Tyr	Thr	Ser	His	Ser 635	Phe	Ala	His	Glu	Thr 640
His	Ile	Thr	Met	Gln 645	Ser	Thr	Val	Gln	Leu 650	Arg	Thr	Glu	Tyr	Asp 655	Pro
His	Thr	His	Val 660	Tyr	Tyr	Thr	Thr	Ala 665	Glu	Pro	Arg	Ser	Glu 670	Ile	Ser
Val	Gln	Pro 675	Val	Thr	Val	Thr	Gln 680	Asp	Asn	Leu	Ser	Cys 685	Gln	Ser	Pro
Glu 690	Ser	Thr	Ser	Ser	Thr	Arg 695	Asp	Leu	Leu	Ser	Gln 700	Phe	Ser	Asp	Ser
Ser 705	Leu	His	Cys	Leu 710	Glu	Pro	Pro	Cys	Thr	Lys 715	Trp	Thr	Leu	Ser	Ser 720
Phe	Ala	Glu	Lys	His 725	Tyr	Ala	Pro	Phe	Leu 730	Leu	Lys	Pro	Lys	Ala 735	Lys
Val	Val	Val	Ile 740	Leu	Leu	Phe	Leu	Gly 745	Leu	Leu	Gly	Val	Ser 750	Leu	Tyr
Gly	Thr	Thr 755	Arg	Val	Arg	Asp	Gly 760	Leu	Asp	Leu	Thr	Asp 765	Ile	Val	Pro
Arg 770	Glu	Thr	Arg	Glu	Tyr	Asp 775	Phe	Ile	Ala	Ala	Gln 780	Phe	Lys	Tyr	Phe
Ser 785	Phe	Tyr	Asn	Met 790	Tyr	Ile	Val	Thr	Gln 795	Lys	Ala	Asp	Tyr	Pro	Asn 800
Ile	Gln	His	Leu 805	Leu	Tyr	Asp	Leu	His 810	Lys	Ser	Phe	Ser	Asn 815	Val	Lys
Tyr	Val	Met 820	Leu	Glu	Glu	Asn	Lys	Gln 825	Leu	Pro	Gln	Met 830	Trp	Leu	His
Tyr	Phe	Arg 835	Asp	Trp	Leu	Gln	Gly 840	Leu	Gln	Asp	Ala	Phe 845	Asp	Ser	Asp
Trp 850	Glu	Thr	Gly	Arg	Ile	Met 855	Pro	Asn	Asn	Tyr	Lys 860	Asn	Gly	Ser	Asp
Asp 865	Gly	Val	Leu	Ala	Tyr 870	Lys	Leu	Leu	Val	Gln 875	Thr	Gly	Ser	Arg	Asp 880
Lys	Pro	Ile	Asp 885	Ile	Ser	Gln	Leu	Thr 890	Lys	Gln	Arg	Leu	Val 895	Asp	Ala
Asp	Gly	Ile 900	Ile	Asn	Pro	Ser	Ala	Phe 905	Tyr	Ile	Tyr	Leu	Thr 910	Ala	Trp
Val	Ser	Asn 915	Asp	Pro	Val	Ala	Tyr 920	Ala	Ala	Ser	Gln 925	Ala	Asn	Ile	Arg
Pro	His	Arg	Pro	Glu	Trp	Val	His	Asp	Lys	Ala	Asp	Tyr	Met	Pro	Glu

930					935					940					
Thr	Arg	Leu	Arg	Ile	Pro	Ala	Ala	Glu	Pro	Ile	Glu	Tyr	Ala	Gln	Phe
945					950					955					960
Pro	Phe	Tyr	Leu	Asn	Gly	Leu	Arg	Asp	Thr	Ser	Asp	Phe	Val	Glu	Ala
				965					970					975	
Ile	Glu	Lys	Val	Arg	Val	Ile	Cys	Asn	Asn	Tyr	Thr	Ser	Leu	Gly	Leu
			980					985					990		
Ser	Ser	Tyr	Pro	Asn	Gly	Tyr	Pro	Phe	Leu	Phe	Trp	Glu	Gln	Tyr	Ile
		995					1000					1005			
Ser	Leu	Arg	His	Trp	Leu	Leu	Leu	Ser	Ile	Ser	Val	Val	Leu	Ala	Cys
	1010					1015					1020				
Thr	Phe	Leu	Val	Cys	Ala	Val	Phe	Leu	Leu	Asn	Pro	Trp	Thr	Ala	Gly
1025					1030					1035					1040
Ile	Ile	Val	Met	Val	Leu	Ala	Leu	Met	Thr	Val	Glu	Leu	Phe	Gly	Met
				1045					1050					1055	
Met	Gly	Leu	Ile	Gly	Ile	Lys	Leu	Ser	Ala	Val	Pro	Val	Val	Ile	Leu
			1060					1065					1070		
Ile	Ala	Ser	Val	Gly	Ile	Gly	Val	Glu	Phe	Thr	Val	His	Val	Ala	Leu
		1075					1080					1085			
Ala	Phe	Leu	Thr	Ala	Ile	Gly	Asp	Lys	Asn	His	Arg	Ala	Met	Leu	Ala
	1090					1095					1100				
Leu	Glu	His	Met	Phe	Ala	Pro	Val	Leu	Asp	Gly	Ala	Val	Ser	Thr	Leu
1105					1110					1115					1120
Leu	Gly	Val	Leu	Met	Leu	Ala	Gly	Ser	Glu	Phe	Asp	Phe	Ile	Val	Arg
				1125					1130					1135	
Tyr	Phe	Phe	Ala	Val	Leu	Ala	Ile	Leu	Thr	Val	Leu	Gly	Val	Leu	Asn
			1140					1145					1150		
Gly	Leu	Val	Leu	Leu	Pro	Val	Leu	Leu	Ser	Phe	Phe	Gly	Pro	Cys	Pro
			1155				1160					1165			
Glu	Val	Ser	Pro	Ala	Asn	Gly	Leu	Asn	Arg	Leu	Pro	Thr	Pro	Ser	Pro
	1170					1175					1180				
Glu	Pro	Pro	Pro	Ser	Val	Val	Arg	Phe	Ala	Val	Pro	Pro	Gly	His	Thr
1185					1190					1195					1200
Asn	Asn	Gly	Ser	Asp	Ser	Ser	Asp	Ser	Glu	Tyr	Ser	Ser	Gln	Thr	Thr
				1205					1210					1215	
Val	Ser	Gly	Ile	Ser	Glu	Glu	Leu	Arg	Gln	Tyr	Glu	Ala	Gln	Gln	Gly
			1220					1225					1230		
Ala	Gly	Gly	Pro	Ala	His	Gln	Val	Ile	Val	Glu	Ala	Thr	Glu	Asn	Pro
			1235				1240					1245			

Val	Phe	Ala	Arg	Ser	Thr	Val	Val	His	Pro	Asp	Ser	Arg	His	Gln	Pro	1250	1255	1260	
Pro	Leu	Thr	Pro	Arg	Gln	Gln	Pro	His	Leu	Asp	Ser	Gly	Ser	Leu	Ser	1265	1270	1275	1280
Pro	Gly	Arg	Gln	Gly	Gln	Gln	Pro	Arg	Arg	Asp	Pro	Pro	Arg	Glu	Gly	1285	1290	1295	
Leu	Arg	Pro	Pro	Pro	Tyr	Arg	Pro	Arg	Arg	Asp	Ala	Phe	Glu	Ile	Ser	1300	1305	1310	
Thr	Glu	Gly	His	Ser	Gly	Pro	Ser	Asn	Arg	Asp	Arg	Ser	Gly	Pro	Val	1315	1320	1325	
Gly	Pro	Val	Leu	Thr	Thr	Leu	Gly	Thr	Gln	Arg	Pro	Pro	Pro	Trp	Ala	1330	1335	1340	
Ala	Leu	Cys	Pro	Ala	Thr	Ala	Ser	Pro	Ser	Pro	Leu					1345	1350	1355	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1356 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Ala	Ser	Ala	Gly	Asn	Ala	Arg	Arg	Gly	Pro	Gly	Gln	Ala	Gly	Arg	1	5	10	15
Arg	Arg	Glu	Ala	Gln	Thr	Asp	Arg	Gly	Thr	Ala	Pro	Arg	Arg	Ala	Gly	20	25	30	
Pro	Gly	Leu	Ser	Ala	Pro	Ala	Gln	Leu	Leu	Arg	Arg	Ala	Phe	Ala	Leu	35	40	45	
Glu	Gln	Ile	Ser	Lys	Gly	Lys	Ala	Thr	Gly	Arg	Lys	Ala	Pro	Leu	Trp	50	55	60	
Leu	Arg	Ala	Lys	Phe	Gln	Arg	Leu	Leu	Phe	Lys	Leu	Gly	Cys	Tyr	Ile	65	70	75	80
Gln	Lys	Asn	Cys	Gly	Lys	Phe	Leu	Val	Val	Gly	Leu	Leu	Ile	Phe	Gly	85	90	95	
Ala	Phe	Ala	Val	Gly	Leu	Lys	Ala	Ala	Asn	Leu	Glu	Thr	Asn	Val	Glu	100	105	110	
Glu	Leu	Trp	Val	Glu	Val	Gly	Gly	Arg	Val	Ser	Arg	Glu	Leu	Asn	Tyr	115	120	125	

Thr	Arg	Gln	Lys	Ile	Gly	Glu	Glu	Ala	Met	Phe	Asn	Pro	Gln	Leu	Met
	130					135					140				
Ile	Gln	Thr	Pro	Lys	Glu	Glu	Gly	Ala	Asn	Val	Leu	Thr	Thr	Glu	Ala
145					150					155					160
Leu	Leu	Gln	His	Leu	Asp	Ser	Ala	Leu	Gln	Ala	Ser	Arg	Val	His	Val
				165					170					175	
Tyr	Met	Tyr	Asn	Arg	Gln	Trp	Lys	Leu	Glu	His	Leu	Cys	Tyr	Lys	Ser
			180					185					190		
Gly	Glu	Leu	Ile	Thr	Glu	Thr	Gly	Tyr	Met	Asp	Gln	Ile	Ile	Glu	Tyr
		195					200					205			
Leu	Tyr	Pro	Cys	Leu	Ile	Ile	Thr	Pro	Leu	Asp	Cys	Phe	Trp	Glu	Gly
	210					215					220				
Ala	Lys	Leu	Gln	Ser	Gly	Thr	Ala	Tyr	Leu	Leu	Gly	Lys	Pro	Pro	Leu
225					230					235					240
Arg	Trp	Thr	Asn	Phe	Asp	Pro	Leu	Glu	Phe	Leu	Glu	Glu	Leu	Lys	Lys
				245					250					255	
Ile	Asn	Tyr	Gln	Val	Asp	Ser	Trp	Glu	Glu	Met	Leu	Asn	Lys	Ala	Glu
			260					265					270		
Val	Gly	His	Gly	Tyr	Met	Asp	Arg	Pro	Cys	Leu	Asn	Pro	Ala	Asp	Pro
		275					280					285			
Asp	Cys	Pro	Ala	Thr	Ala	Pro	Asn	Lys	Asn	Ser	Thr	Lys	Pro	Leu	Asp
	290					295					300				
Val	Ala	Leu	Val	Leu	Asn	Gly	Gly	Cys	Gln	Gly	Leu	Ser	Arg	Lys	Tyr
305					310					315					320
Met	His	Trp	Gln	Glu	Glu	Leu	Ile	Val	Gly	Gly	Thr	Val	Lys	Asn	Ala
				325					330					335	
Thr	Gly	Lys	Leu	Val	Ser	Ala	His	Ala	Leu	Gln	Thr	Met	Phe	Gln	Leu
			340					345					350		
Met	Thr	Pro	Lys	Gln	Met	Tyr	Glu	His	Phe	Arg	Gly	Tyr	Asp	Tyr	Val
		355					360					365			
Ser	His	Ile	Asn	Trp	Asn	Glu	Asp	Arg	Ala	Ala	Ala	Ile	Leu	Glu	Ala
		370				375					380				
Trp	Gln	Arg	Thr	Tyr	Val	Glu	Val	Val	His	Gln	Ser	Val	Ala	Pro	Asn
385					390					395					400
Ser	Thr	Gln	Lys	Val	Leu	Pro	Phe	Thr	Thr	Thr	Thr	Leu	Asp	Asp	Ile
				405				410						415	
Leu	Lys	Ser	Phe	Ser	Asp	Val	Ser	Val	Ile	Arg	Val	Ala	Ser	Gly	Tyr
			420					425					430		
Leu	Leu	Met	Leu	Ala	Tyr	Ala	Cys	Leu	Thr	Met	Leu	Arg	Trp	Asp	Cys

435					440					445					
Ser	Lys	Ser	Gln	Gly	Ala	Val	Gly	Leu	Ala	Gly	Val	Leu	Leu	Val	Ala
450						455					460				
Leu	Ser	Val	Ala	Ala	Gly	Leu	Gly	Leu	Cys	Ser	Leu	Ile	Gly	Ile	Ser
465					470					475					480
Phe	Asn	Ala	Ala	Thr	Thr	Gln	Val	Leu	Pro	Phe	Leu	Ala	Leu	Gly	Val
				485					490					495	
Gly	Val	Asp	Asp	Val	Phe	Leu	Leu	Ala	His	Ala	Phe	Ser	Glu	Thr	Gly
			500					505					510		
Gln	Asn	Lys	Arg	Ile	Pro	Phe	Glu	Asp	Arg	Thr	Gly	Glu	Cys	Leu	Lys
		515					520					525			
Arg	Thr	Gly	Ala	Ser	Val	Ala	Leu	Thr	Ser	Ile	Ser	Asn	Val	Thr	Ala
	530					535					540				
Phe	Phe	Met	Ala	Ala	Leu	Ile	Pro	Ile	Pro	Ala	Leu	Arg	Ala	Phe	Ser
545					550					555					560
Leu	Gln	Ala	Ala	Val	Val	Val	Val	Phe	Asn	Phe	Ala	Met	Val	Leu	Leu
				565					570					575	
Ile	Phe	Pro	Ala	Ile	Leu	Ser	Met	Asp	Leu	Tyr	Arg	Arg	Glu	Asp	Arg
			580					585					590		
Arg	Leu	Asp	Ile	Phe	Cys	Cys	Leu	Thr	Ser	Pro	Cys	Val	Ser	Arg	Val
		595					600					605			
Ile	Gln	Val	Glu	Pro	Gln	Ala	Tyr	Thr	Glu	Pro	His	Ser	Asn	Thr	Arg
	610					615					620				
Tyr	Ser	Pro	Pro	Pro	Pro	Tyr	Thr	Ser	His	Ser	Phe	Ala	His	Glu	Thr
625					630					635				640	
His	Ile	Thr	Met	Gln	Ser	Thr	Val	Gln	Leu	Arg	Thr	Glu	Tyr	Asp	Pro
				645					650					655	
His	Thr	His	Val	Tyr	Tyr	Thr	Thr	Ala	Glu	Pro	Arg	Ser	Glu	Ile	Ser
			660					665					670		
Val	Gln	Pro	Val	Thr	Val	Thr	Gln	Asp	Asn	Leu	Ser	Cys	Gln	Ser	Pro
		675					680					685			
Glu	Ser	Thr	Ser	Ser	Thr	Arg	Asp	Leu	Leu	Ser	Gln	Phe	Ser	Asp	Ser
	690					695					700				
Ser	Leu	His	Cys	Leu	Glu	Pro	Pro	Cys	Thr	Lys	Trp	Thr	Leu	Ser	Ser
705					710					715					720
Phe	Ala	Glu	Lys	His	Tyr	Ala	Pro	Phe	Leu	Leu	Lys	Pro	Lys	Ala	Lys
				725					730					735	
Val	Val	Val	Ile	Leu	Leu	Phe	Leu	Gly	Leu	Leu	Gly	Val	Ser	Leu	Tyr
			740					745					750		

Gly	Thr	Thr	Arg	Val	Arg	Asp	Gly	Leu	Asp	Leu	Thr	Asp	Ile	Val	Pro
		755					760					765			
Arg	Glu	Thr	Arg	Glu	Tyr	Asp	Phe	Ile	Ala	Ala	Gln	Phe	Lys	Tyr	Phe
	770					775					780				
Ser	Phe	Tyr	Asn	Met	Tyr	Ile	Val	Thr	Gln	Lys	Ala	Asp	Tyr	Pro	Asn
785					790					795					800
Ile	Gln	His	Leu	Leu	Tyr	Asp	Leu	His	Lys	Ser	Phe	Ser	Asn	Val	Lys
				805					810					815	
Tyr	Val	Met	Leu	Glu	Glu	Asn	Lys	Gln	Leu	Pro	Gln	Met	Trp	Leu	His
			820					825					830		
Tyr	Phe	Arg	Asp	Trp	Leu	Gln	Gly	Leu	Gln	Asp	Ala	Phe	Asp	Ser	Asp
		835					840					845			
Trp	Glu	Thr	Gly	Arg	Ile	Met	Pro	Asn	Asn	Tyr	Lys	Asn	Gly	Ser	Asp
	850					855					860				
Asp	Gly	Val	Leu	Ala	Tyr	Lys	Leu	Leu	Val	Gln	Thr	Gly	Ser	Arg	Asp
865					870					875					880
Lys	Pro	Ile	Asp	Ile	Ser	Gln	Leu	Thr	Lys	Gln	Arg	Leu	Val	Asp	Ala
				885					890					895	
Asp	Gly	Ile	Ile	Asn	Pro	Ser	Ala	Phe	Tyr	Ile	Tyr	Leu	Thr	Ala	Trp
			900					905					910		
Val	Ser	Asn	Asp	Pro	Val	Ala	Tyr	Ala	Ala	Ser	Gln	Ala	Asn	Ile	Arg
		915					920					925			
Pro	His	Arg	Pro	Glu	Trp	Val	His	Asp	Lys	Ala	Asp	Tyr	Met	Pro	Glu
	930					935					940				
Thr	Arg	Leu	Arg	Ile	Pro	Ala	Ala	Glu	Pro	Ile	Glu	Tyr	Ala	Gln	Phe
945					950					955					960
Pro	Phe	Tyr	Leu	Asn	Gly	Leu	Arg	Asp	Thr	Ser	Asp	Phe	Val	Glu	Ala
				965					970					975	
Ile	Glu	Lys	Val	Arg	Val	Ile	Cys	Asn	Asn	Tyr	Thr	Ser	Leu	Gly	Leu
			980					985					990		
Ser	Ser	Tyr	Pro	Asn	Gly	Tyr	Pro	Phe	Leu	Phe	Trp	Glu	Gln	Tyr	Ile
		995					1000					1005			
Ser	Leu	Arg	His	Trp	Leu	Leu	Leu	Ser	Ile	Ser	Val	Val	Leu	Ala	Cys
	1010					1015					1020				
Thr	Phe	Leu	Val	Cys	Ala	Val	Phe	Leu	Leu	Asn	Pro	Trp	Thr	Ala	Gly
1025					1030					1035					1040
Ile	Ile	Val	Met	Val	Leu	Ala	Leu	Met	Thr	Val	Glu	Leu	Phe	Gly	Met
				1045					1050					1055	
Met	Gly	Leu	Ile	Gly	Ile	Lys	Leu	Ser	Ala	Val	Pro	Val	Val	Ile	Leu

1060					1065					1070					
Ile	Ala	Ser	Val	Gly	Ile	Gly	Val	Glu	Phe	Thr	Val	His	Val	Ala	Leu
	1075						1080					1085			
Ala	Phe	Leu	Thr	Ala	Ile	Gly	Asp	Lys	Asn	His	Arg	Ala	Met	Leu	Ala
	1090					1095					1100				
Leu	Glu	His	Met	Phe	Ala	Pro	Val	Leu	Asp	Gly	Ala	Val	Ser	Thr	Leu
1105						1110					1115				1120
Leu	Gly	Val	Leu	Met	Leu	Ala	Gly	Ser	Glu	Phe	Asp	Phe	Ile	Val	Arg
				1125					1130					1135	
Tyr	Phe	Phe	Ala	Val	Leu	Ala	Ile	Leu	Thr	Val	Leu	Gly	Val	Leu	Asn
			1140					1145					1150		
Gly	Leu	Val	Leu	Leu	Pro	Val	Leu	Leu	Ser	Phe	Phe	Gly	Pro	Cys	Pro
	1155						1160					1165			
Glu	Val	Ser	Pro	Ala	Asn	Gly	Leu	Asn	Arg	Leu	Pro	Thr	Pro	Ser	Pro
	1170					1175					1180				
Glu	Pro	Pro	Pro	Ser	Val	Val	Arg	Phe	Ala	Val	Pro	Pro	Gly	His	Thr
1185						1190					1195				1200
Asn	Asn	Gly	Ser	Asp	Ser	Ser	Asp	Ser	Glu	Tyr	Ser	Ser	Gln	Thr	Thr
				1205					1210					1215	
Val	Ser	Gly	Ile	Ser	Glu	Glu	Leu	Arg	Gln	Tyr	Glu	Ala	Gln	Gln	Gly
			1220					1225					1230		
Ala	Gly	Gly	Pro	Ala	His	Gln	Val	Ile	Val	Glu	Ala	Thr	Glu	Asn	Pro
	1235						1240					1245			
Val	Phe	Ala	Arg	Ser	Thr	Val	Val	His	Pro	Asp	Ser	Arg	His	Gln	Pro
	1250					1255					1260				
Pro	Leu	Thr	Pro	Arg	Gln	Gln	Pro	His	Leu	Asp	Ser	Gly	Ser	Leu	Ser
1265						1270					1275				1280
Pro	Gly	Arg	Gln	Gly	Gln	Gln	Pro	Arg	Arg	Asp	Pro	Pro	Arg	Glu	Gly
				1285					1290					1295	
Leu	Arg	Pro	Pro	Pro	Tyr	Arg	Pro	Arg	Arg	Asp	Ala	Phe	Glu	Ile	Ser
			1300					1305					1310		
Thr	Glu	Gly	His	Ser	Gly	Pro	Ser	Asn	Arg	Asp	Arg	Ser	Gly	Pro	Val
		1315					1320					1325			
Gly	Pro	Val	Leu	Thr	Thr	Leu	Gly	Thr	Gln	Arg	Pro	Pro	Pro	Trp	Ala
1330						1335					1340				
Ala	Leu	Cys	Pro	Ala	Thr	Ala	Ser	Pro	Ser	Pro	Leu				
1345						1350					1355				

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9042 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GATCCTGAAT	TGAGAAATAT	AGATTGAAAC	AGAATTCATT	ACCATTTAAG	CAATCATTAT	60
TTATGGGGGC	GTAATGCGCC	TCCGAGTAGG	CAATGCTTTT	CTTGACATTG	TTACTAAGAA	120
TTGTGAATGA	TATTTGGGCG	TGGATCAACG	CCGATTAAAA	GCTGCTTTTG	CTTCCAGGCG	180
GCCAGAGAAG	AGATCCAAAC	TTCAACTCCA	GCCATAAAAG	CAACAACATT	TCCGTCTCCC	240
CCTTGTAGCT	CCCCTTCCTC	CGGCTCTTCC	ACTCTCCACG	AAACGGCAAA	TGAAGCTCTC	300
AAAGCGAACT	GTGCTTCGCT	GGTGGTCCAT	TGGCAGCTGC	CGCCACACAG	GCGCTGCTTT	360
TGTGTGTGTG	TGTAATATCA	ATCTTGCTCT	CCCTCTCTTT	TTATCTCTCT	TGGGAATTGG	420
AGCTGCATGC	GAATTGAGCG	ACAGCAAAAC	GAAGTGCAAG	TCATTGAGAG	GAGAGCAAAA	480
ACTCGAGCGC	AAGCCAAAGA	TAGCGCAATC	TGGGGAGAGC	GAAATAAAGC	TAAAATATGC	540
ATGTTGGAGA	AAAAATGCCG	CCCATGTCGC	CAAATGCGC	CACACGCAGA	GTGAGCGGGC	600
GGAGGTGGGA	GTAATGGAAA	GGGCGATGAG	GGAACGATTA	GCTTGAAGAG	AGAGAACAAC	660
AAATGAATGT	GCTGCAACGT	TAGTTCAGGT	GAGCGCGTTA	GAGAGAGAGT	TGTTGTTTTT	720
TGATTGTAAT	AGCTCGCTTG	GTGGTGGGTC	CACATTCACA	TCTCCCTCTC	CCACTCTTTC	780
TCCCCGAAAG	AGAGAGCGGG	AGCGAAGGGG	CACGAGGGGA	GCACGATGAC	TATGCAGTTG	840
CATTCAATTT	GAATTTCCAT	GGTGCTGATG	ATTCGAGCGC	CAATTTTTTC	GAAGAGTTCT	900
TATTTGTTTA	CTTCGTTGTT	GTTGCCTCAA	TTGGAAAGGG	AAAATGTGGA	ATGCGGAGAA	960
ACACCAGAAG	CAAATGCATT	TCCATTCATA	AATCCAAAGA	AGTTTTAAAG	ATAACATGTC	1020
ATTTGGCTTA	AGTTCGTGGT	GCACAAAAAA	GATCGGTTTG	CGGTTGTCGC	ATGAAATGAG	1080
TTTATTCCAT	TGGTATATTA	TTATTCAGAA	ATTAAAAAAA	AACTTGTTTA	GTCTATTTTT	1140
TTTTTTTAAA	TAAAAA AAAA	AAATTCTTTT	ATAAGTCGAT	TTAGAGTAA	ATATTTAAAG	1200
ACTACGTCTA	ATAACATAT	AATTTGTTCT	GTGTTTTAAT	TTGCCGGCAA	AAACAAACCT	1260
ACTTGTGTGG	TCCTCGCACA	CTCATAACCC	CTCGCATATT	TGAGATTCAT	GGGGCAAGAG	1320
GCTGCAAAAA	CAATGGAAAG	GGAAAAGCAG	AAACATCCTG	CCGCTCATAA	TTTAGCATCG	1380

GAACATGCAA	AAACAGACAT	CATCGCATGG	GGCAGCAGCA	ACAGCCATAA	AACCAACACG	1440
AGCAATGTAA	AGCTAACAAA	TTTGCCAACA	GTTCGCGGCA	CGGCTACACA	CACACACATG	1500
CATGCGCAGC	CTGCCACGCA	CGCGCTTCCC	CCAAACAAAT	ACACACACAC	ACACTGAGAC	1560
GAAAGCTCCA	TTGGGCAGCG	CTGCCGACGC	TGAAGGCCGA	CATCGGCAGA	GCTGAACGTT	1620
TGGGTAGGGG	ACCACCCACA	TCGCTTGGCG	GTTTCAGTTT	AATGAAGGCA	GAAACAAATT	1680
TATTTTTTGGG	TGGTCCACAC	TGCAGCGAAA	ATAAACTACA	GTGGCAACAA	CAAACCAGCA	1740
GCCAAGGCAC	TTTGGGTGGT	CCATGCAAAA	AAAAAACAAA	TTACGGCATG	CGAATAACAA	1800
TAGAAATTAG	CGCTCTCGTG	GCGGAGCTAT	TTGGGTATAT	TAGAGCTACA	TATTTTATTT	1860
GTTTATAAAA	AGTATAAATG	TAAACAATGA	GTTCCAAGCA	TTAAGTCCGT	ATGCTCAACA	1920
ATTACATTAT	CATTATTATT	ATCACTTAAA	TATTTACAAA	GGATATTTAA	ACAGTAATAG	1980
ATATATATTT	TATTTCTTAA	TTTCTGTAA	CATATGTATT	TACATTGGTA	GTATTCTTT	2040
ATTTTGCAAC	AAGCATTCAT	AAATTTTATA	TAACAAACTT	GGTATTTTCT	CGGAAAAACT	2100
CCTGAATCAC	CCCTCGGTAT	TTTGTGCGTT	GAGCTATCGT	TAAAGCAGCC	CTCGCAGAGA	2160
GCGTTCTCAA	ACCAAAATGG	CCGCACACGA	AACAAGAGAG	CGAGTGAGAG	TAGGGAGAGC	2220
GTCTGTGTTG	TGTGTTGAGT	GTCGCCCACG	CACACAGGCG	CAAAACAGTG	CACACAGACG	2280
CCCGCTGGGC	AAGAGAGAGT	GAGAGAGAGA	AACAGCGGCG	CGCGCTCGCC	TAATGAAGTT	2340
GTTGGCCTGG	CTGGCGTGCC	GCATCCACGA	GATACAGATA	CATCTCTCAG	ACTGCGTGCG	2400
ATCCTCGAAC	GAAACGGTTG	TAAGTGCGGA	GCGCGACGAC	TTGTTATTCTG	TATTTCCGAC	2460
TACTGGCACT	CTCTGTGTGT	GGTATACTAA	CAAGATAGAT	ATCACAGAAC	TCGTGGAAAA	2520
GCTAAGATAT	TGTACCTCAC	GGATGCGAGG	CGAAGTTCAT	GGATTAAATG	CCAGGCAACA	2580
ACAAAAGCCA	GCCAACCAGC	CAGTGTTTGT	GTGTGTGCGT	CGCCAAGTGC	AAAGTAAAGT	2640
AAAGGTAAAA	GAGCGAAAGG	CGAGAGAGAA	AACCGAATAC	GTGAGTCGTC	CGACTGCCGC	2700
TTTTCCATGT	GTAAAAGATC	TGTGAAAATT	CTGTCAAATT	CCCCTGAGAA	ATTGTGCCCA	2760
AGATAAAACC	CGAAAACCGC	GTTTAAATCG	TCGAAAAAAC	CCAGCAAAG	CGAAGCCAGC	2820
AATCACAACA	AAACAACATA	ACGAGAGCTC	AGATACACAG	CGTGCTCAGT	GAGTGAGCGA	2880
GAGAGCGCGG	GAGAGAGCGT	CTCTTGATTT	AAAATACAAA	ATAATTAAAA	ATAAAAATGC	2940
GGAATGCAGT	GCAAAATGCA	GCCAAACAAA	ATACGAGATT	CCAATAACAA	TTAATCGAAC	3000
CGAAAGTCCA	CGAACAATCC	GCACACTGTC	TCCCAAGTCT	CAGTTCTCAG	GACGCAGACG	3060
AACGGCAGGC	ACTGTAGAAA	GACCGATTCC	GCAGCACACT	CCCATCTGCA	CATCTCCGCC	3120

ACGCGATTCC	GTCCGGAATC	TGGCTATAAA	CATAACCATA	ATGGACCGCG	ACAGCCTCCC	3180
ACGCGTTCCG	GACACACACG	GCGATGTGGT	CGATGAGAAA	TTATTCTCGG	ATCTTTACAT	3240
ACGCACCAGC	TGGGTGGACG	CCCAAGTGGC	GCTCGATCAG	ATAGATAAAG	TGAGTGCCCA	3300
ACTACAGTGA	ACTTTCACCTG	TGAAGGATAG	CCATGTGTTG	AATTCAATAA	TATTCTTGAT	3360
CGTATTTCGGA	GGATCCAATT	TTAATGCGTA	TTTTATGGCA	GTGGAGCAAG	GCGGGGGAAT	3420
CTAAAAA	AACTAAACGC	TAAATTCCGT	ATTTTTGTG	CATTTTTCAG	GGCAAAGCGC	3480
GTGGCAGCCG	CACGGCGATC	TATCTGCGAT	CAGTATTCCA	GTCCCACCTC	GAAACCCTCG	3540
GCAGCTCCGT	GCAAAGCAC	GCGGGCAAGG	TGCTATTCGT	GGCTATCCTG	GTGCTGAGCA	3600
CCTTCTGCGT	CGGCCTGAAG	AGCGCCCAGA	TCCACTCCAA	GGTGACCAG	CTGTGGATCC	3660
AGGAGGGCGG	CCGGCTGGAG	GCGGAACTGG	CCTACACACA	GAAGACGATC	GGCGAGGACG	3720
AGTCGGCCAC	GCATCAGCTG	CTCATTCAGA	CGACCCACGA	CCCGAACGCC	TCCGTCCTGC	3780
ATCCGCAGGC	GCTGCTTGCC	CACCTGGAGG	TCCTGGTCAA	GGCCACCGCC	GTCAAGGTGC	3840
ACCTCTACGA	CACCGAATGG	GGGCTGCGCG	ACATGTGCAA	CATGCCGAGC	ACGCCCTCCT	3900
TCGAGGGCAT	CTACTACATC	GAGCAGATCC	TGCGCCACCT	CATTCCGTGC	TCGATCATCA	3960
CGCCGCTGGA	CTGTTTCTGG	GAGGGAAGCC	AGCTGTTGGG	TCCGGAATCA	GCGGTCGTTA	4020
TACCGTAAGT	AGTTAATATG	TAGTTAATAG	CCACATCTTA	TAGATTCTAA	AGTGAACGTA	4080
TCCCTTATGA	CCATATCCTT	TTGCATGATC	TACTTTAACC	CACAGTACTT	CTCTATTTCAT	4140
ATTAAGGAAT	TAATAAAGTA	CTTACTTTGC	GCTTACCTTT	ATTAAATACG	ATAGCTTATC	4200
TTTATAAACT	TGCTATCAAG	TCGAAAGATA	AACGTGACAA	GAGTATCTTT	GTACTTATCC	4260
CAGTTGCTTA	CCATCGTAAA	TAATCTTCTT	ATTAATAAAT	ATTCGTAAAT	AAATATTCTT	4320
AACTCAACAA	ATCCATCTTT	ATTATTGTTA	CTCCTCTACA	GAGGCCTCAA	CCAACGACTC	4380
CTGTGGACCA	CCCTGAATCC	CGCCTCTGTG	ATGCAGTATA	TGAAACAAAA	GATGTCCGAG	4440
GAAAAGATCA	GCTTCGACTT	CGAGACCGTG	GAGCAGTACA	TGAAGCGTGC	GGCCATTGGC	4500
AGTGGCTACA	TGGAGAAGCC	CTGCCTGAAC	CCACTGAATC	CCAATTGCCC	GGACACGGCA	4560
CCGAACAAGA	ACAGCACCCA	GCCGCCGGAT	GTGGGAGCCA	TCCTGTCCGG	AGGCTGCTAC	4620
GGTTATGCCG	CGAAGCACAT	GCACTGGCCG	GAGGAGCTGA	TTGTGGGCGG	ACGGAAGAGG	4680
AACCGCAGCG	GACACTTGAG	GAAGGCCAG	GCCCTGCAGT	CGGTGGTGCA	GCTGATGACC	4740
GAGAAGGAAA	TGTACGACCA	GTGGCAGGAC	AACTACAAGG	TGCACCATCT	TGGATGGACG	4800
CAGGAGAAGG	CAGCGGAGGT	TTTGAACGCC	TGGCAGCGCA	ACTTTTCGCG	GGAGGTGGAA	4860

CAGCTGCTAC	GTAAACAGTC	GAGAATTGCC	ACCAACTACG	ATATCTACGT	G TTCAGCTCG	4920
GCTGCACTGG	ATGACATCCT	GGCCAAGTTC	TCCCATCCCA	GCGCCTTGTC	CATTGTCATC	4980
GGCGTGGCCG	TCACCGTTTT	GTATGCCTTT	TGCACGCTCC	TCCGCTGGAG	GGACCCCGTC	5040
CGTGGCCAGA	GCAGTGTGGG	CGTGGCCGGA	GTTCTGCTCA	TGTGCTTCAG	TACCGCCGCC	5100
GGATTGGGAT	TGTCAGCCCT	GCTCGGTATC	GTTTTCAATG	CGCTGACCGC	TGCCTATGCG	5160
GAGAGCAATC	GGCGGGAGCA	GACCAAGCTG	ATTCTCAAGA	ACGCCAGCAC	CCAGGTGGTT	5220
CCGTTTTTGG	CCCTTGGTCT	GGGCGTCGAT	CACATCTTCA	TAGTGGGACC	GAGCATCCTG	5280
TTCAGTGCCT	GCAGACCCGC	AGGATCCTTC	TTTGCGGCCG	CCTTTATTCC	GGTGCCGGCT	5340
TTGAAGGTAT	TCTGTCTGCA	GGCTGCCATC	GTAATGTGCT	CCAATTTGGC	AGCGGCTCTA	5400
TTGGTTTTTC	CGGCCATGAT	TTCGTTGGAT	CTACGGAGAC	GTACCGCCGG	CAGGGCGGAC	5460
ATCTTCTGCT	GCTGTTTTCC	GGTGTGGAAG	GAACAGCCGA	AGGTGGCACC	TCCGGTGCTG	5520
CCGCTGAACA	ACAACAACGG	GCGCGGGGCC	CGGCATCCGA	AGAGCTGCAA	CAACAACAGG	5580
GTGCCGCTGC	CCGCCCAGAA	TCCTCTGCTG	GAACAGAGGG	CAGACATCCC	TGGGAGCAGT	5640
CACTCACTGG	CGTCCTTCTC	CCTGGCAACC	TTCGCCTTTC	AGCACTACAC	TCCCTTCCTC	5700
ATGCGCAGCT	GGGTGAAGTT	CCTGACCGTT	ATGGGTTTCC	TGGCGGCCCT	CATATCCAGC	5760
TTGTATGCCT	CCACGCGCCT	TCAGGATGGC	CTGGACATTA	TTGATCTGGT	GCCCAAGGAC	5820
AGCAACGAGC	ACAAGTTCCT	GGATGCTCAA	ACTCGGCTCT	TTGGCTTCTA	CAGCATGTAT	5880
GCGGTTACCC	AGGGCAACTT	TGAATATCCC	ACCCAGCAGC	AGTTGCTCAG	GGACTACCAT	5940
GATTCCTTTG	TGCGGGTGCC	ACATGTGATC	AAGAATGATA	ACGGTGGACT	GCCGGACTTC	6000
TGGCTGCTGC	TCTTCAGCGA	GTGGCTGGGT	AATCTGCAAA	AAGATATTCTG	ACGAGGAATA	6060
CCGCGACGGA	CGGCTGGACC	AAGGAGTGCT	GGTTCCCAAA	CGCCAGCAGC	GATCGCCATC	6120
CTGGCCTACA	AGCTAATCGT	GCAAACCGGC	CATGTGGACA	ACCCCGTGGA	CAAGGAACTG	6180
GTGCTCACCA	ATCGCCTGGT	CAACAGCGAT	GGCATCATCA	ACCAACGCGC	CTTCTACAAC	6240
TATCTGTCGG	CATGGGCCAC	CAACGACGTC	TTCGCCTACG	GAGCTTCTCA	GGTGGGTCTT	6300
CTTATTAAAT	TAAATTAAAT	TAAATTAAAT	TAGATCGCCT	TAGTTCTCCT	CATATGTACA	6360
TACATATTAT	AACTTATCGC	ACTCCAAAGT	TAAAGATTAC	TAAATGTGTG	TGTATCTTTA	6420
TTCTTACAGG	GCAAATTGTA	TCCGGAACCG	CGCCAGTATT	TTCACCAACC	CAACGAGTAC	6480
GATCTTAAGA	TACCCAAGAG	TCTGCCATTG	GTCTACGCTC	AGATGCCCTT	TTACCTCCAC	6540
GGACTAACAG	ATACCTCGCA	GATCAAGACC	CTGATAGGTC	ATATTCGCGA	CCTGAGCGTC	6600

AAGTACGAGG	GCTTCGGCCT	GCCCAACTAT	CCATCGGGTG	AGTCGGAAAT	GAGTACTTCA	6660
TACATGGGGC	CCAACTAACA	GTCGATTTAT	TTATCGCCAG	GCATTCCCTT	CATCTTCTGG	6720
GAGCAGTACA	TGACCCTGCG	CTCCTCACTG	GCCATGATCC	TGGCCTGCGT	GCTACTCGCC	6780
GCCCTGGTGC	TGGTCTCCCT	GCTCCTGCTC	TCCGTTTGGG	CCGCCGTTCT	CGTGATCCTC	6840
AGCGTTCTGG	CCTCGCTGGC	CCAGATCTTT	GGGGCCATGA	CTCTGCTGGG	CATCAAACCTC	6900
TCGGCCATTC	CGGCAGTCAT	ACTCATCCTC	AGCGTGGGCA	TGATGCTGTG	CTTCAATGTG	6960
CTGATATCAC	TGGTGAGTCT	TCATTTCTGG	CTGGACCATT	AAGAGCTTCG	GAGTGAGTCT	7020
TCATTTCTGG	CTGGACCATT	AAGAGCTTCG	GAGTGAGTCT	TCATTTCTGG	CTGGACCATT	7080
AAGAGCTTCG	GATTTTCCAG	AGATATCCCA	AGACTTTTCA	TTGGATCCTC	TTCAGCACAC	7140
ATTAATTGCT	TATCTTTCCG	ATTCTAGGGC	TTCATGACAT	CCGTTGGCAA	CCGACAGCGC	7200
CGCGTCCAGC	TGAGCATGCA	GATGTCCCTG	GGACCACTTG	TCCACGGCAT	GCTGACCTCC	7260
GGAGTGGCCG	TGTTCATGCT	CTCCACGTGC	CCCTTTGAGT	TTGTGATCCG	GCACTTCTGC	7320
TGGCTTCTGC	TGGTGGTCTT	ATGCGTTGGC	GCCTGCAACA	GCCTTTTGGT	GTTCCCCATC	7380
CTACTGAGCA	TGGTGGGACC	GGAGGCGGAG	CTGGTGCCGC	TGGAGCATCC	AGACCGCATA	7440
TCCACGCCCT	CTCCGCTGCC	CGTGCGCAGC	AGCAAGAGAT	CGGGCAAATC	CTATGTGGTG	7500
CAGGGATCGC	GATCCTCGCG	AGGCAGCTGC	CAGAAGTCGC	ATCACCACCA	CCACAAAGAC	7560
CTTAATGATC	CATCGCTGAC	GACGATCACC	GAGGAGCCGC	AGTCGTGGAA	GTCCAGCAAC	7620
TCGTCCATCC	AGATGCCCAA	TGATTGGACC	TACCAGCCGC	GGGAACAGCG	ACCCGCCTCC	7680
TACGCGGCCC	CGCCCCCGC	CTATCACAAG	GCCGCCGCCC	AGCAGCACCA	CCAGCATCAG	7740
GGCCCGCCCA	CAACGCCCCC	GCCTCCCTTC	CCGACGGCCT	ATCCGCCGGA	GCTGCAGAGC	7800
ATCGTGGTGC	AGCCGGAGGT	GACGGTGGAG	ACGACGCACT	CGGACAGCAA	CACCACCAAG	7860
GTGACGGCCA	CGGCCAACAT	CAAGGTGGAG	CTGGCCATCC	CGGCAGGCGG	TGCGCAGCTA	7920
TAACTTTACG	AGTTAGCACT	AGCACTAGTT	CCTGTAGCTA	TTAGGACGTA	TCTTTAGACT	7980
CTAGCCTAAG	CCGTAACCCT	ATTTGTATCT	GTAAAATCGA	TTTGTCCAGC	GGGTCTGCTG	8040
AGGATTTTCGT	TCTCATGGAT	TCTCATGGAT	TCTCATGGAT	GCTTAAATGG	CATGGTAATT	8100
GGCAAAATAT	CAATTTTTGT	GTCTCAAAAA	GATGCATTAG	CTTATGGTTT	CAAGATACAT	8160
TTTTAAAGAG	TCCGCCAGAT	ATTTATATAA	AAAAAATCCA	AAATCGACGT	ATCCATGAAA	8220
ATTGAAAAGC	TAAGCAGACC	CGTATGTATG	TATATGTGTA	TGCATGTTAG	TTAATTTCCC	8280
GAAGTCCGGT	ATTTATAGCA	GCTGCCTTCC	GCGCCCCCCT	TCCCTTGAAA	TGAACACCCT	8340

TCCAGCCACG	CCCCACCGCC	CCTCTGCGTA	GCAGCTTTGT	ATGTATGTAG	TATGCTAGCA	8400
CCTAAGGAAT	ACTTAAACTT	AGAGATATTT	ATTGTAACAC	ACGCAAAACA	CACACAATGT	8460
ACTTACATAT	AATTCAATGC	GAGATTCACC	CACACAAAAA	GGAAACACAA	CAAAC TAGTA	8520
ATTGTAGCTC	GTAATTTAGT	TTAAATATGT	TACATAAAAC	ACAAGGACTT	GAACCAAAAT	8580
AGTATCGCTT	AAACGGAAAC	GAGAGAAACG	AGAAAAAATA	ACTATTACTT	AATCAACTAC	8640
AAGAGAGATA	TCCCTCCTCC	CCTAACCGTA	CTTACAACCA	AAATAAAACA	AGAGTATAAG	8700
CATAAAAATG	GAAAACGAAG	CGAGGAACGA	TTGTAAACGC	GGTCATTTAT	CCTGTACATT	8760
TGTTGCCCGA	AGACTGACTG	TCTTTTTTTT	AATAAAAATA	TATATTATAC	AGTTTTTTTAA	8820
AAGCGAAATT	CATGACTTTT	TTTTAACAGT	GAGCAGAGAA	CAAAGAAAC	GGAAGTTTTC	8880
GCTGTATCAA	TAAAAAGATT	CCATTTTTTT	AATAAATTGT	AAAAATCCTA	AAAAAAAGAA	8940
GACTACAAAA	GTTTAAATTT	TTATACGTTA	TTGATAAACT	TTTATACACG	AAAATACTTG	9000
TACTTAGCTA	TGATCAACTC	CTTGGCTTAA	GTCTCGGGTA	AG		9042

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ile	Ile	Thr	Pro	Leu	Asp	Cys	Phe	Trp	Glu	Gly
1				5					10	

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Leu	Ile	Val	Gly	Gly
1				5

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Pro Phe Phe Trp Glu Gln Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGACGAATTC AAGTCACATT GG

22

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGACGAATTC CTCCCAAACA TC

22

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGACGAATTC TGATGTTTGG GA

22

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGACGAATTC TGATGTTTGG GA

22

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATACCAGCC AAGCTTGTCG GCCATGCAT

29